

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:19:47 ; Search time 10.1722 Seconds
(without alignments)
151.341 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	376	1 HHECDJ	heat shock protein
2	86	100.0	376	2 G90630	DnaJ protein [impo
3	86	100.0	376	2 G85481	chaperone with Dna
4	86	100.0	379	2 AF0503	DnaJ protein [impo
5	86	100.0	379	2 AB0058	chaperone protein
6	86	100.0	394	2 C64112	heat shock protein
7	83	96.5	381	2 D82270	dnaJ protein VC085
8	82	95.3	392	2 S15295	nolC protein - Rhi
9	75	87.2	377	2 F84947	dnaJ protein [impo
10	75	87.2	377	2 JC5609	heat shock protein
11	73	84.9	373	2 D81242	DnaJ protein NMA02
12	73	84.9	375	2 B47042	heat shock protein
13	73	84.9	377	2 D97373	chaperone protein
14	73	84.9	377	2 AD2591	molecular chaperon
15	73	84.9	377	2 AC3502	chaperone protein
16	64	74.4	367	2 I40843	heat shock protein
17	64	74.4	370	2 C71729	dnaJ protein (dnaJ
18	63	73.3	376	2 E70361	chaperone DnaJ - A
19	62	72.1	190	2 B35388	heat shock protein
20	62	72.1	377	2 A83052	DnaJ protein PA476
21	60	69.8	373	2 H97728	dnaJ protein [impo
22	58	67.4	379	2 H86902	DnaJ protein [impo
23	58	67.4	379	2 A47079	heat shock protein
24	58	67.4	385	2 C87250	dnaJ protein [impo
25	57	66.3	352	2 A49210	heat shock protein
26	57	66.3	364	2 D70164	heat shock protein
27	57	66.3	376	2 AD1621	heat shock protein
28	57	66.3	377	2 T43739	heat shock protein
29	57	66.3	377	2 AH1258	heat shock protein

RESULT 1

HHECDJ

heat shock protein dnaJ - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004

C;Accession: A92572; A26298; S40537; G64721; A26299

R;Bardwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zylicz, M.; Georgopoulos, C.

J. Biol. Chem. 261, 1782-1785, 1986

A;Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.

A;Reference number: A92572; MUID:86111850; PMID:3003085

A;Accession: A92572

A;Molecule type: DNA

A;Residues: 1-376 <BAR>

A;Cross-references: UNIPROT:P08622; GB:M12565; NID:g145767; PIDN:AAA23693.1; PID:g145769

A;Experimental source: strain K12

R;Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.

J. Biol. Chem. 261, 1778-1781, 1986

A;Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the g

A;Reference number: A26298; MUID:86111849; PMID:3003084

A;Accession: A26298

A;Molecule type: DNA

A;Residues: 1-376 <OHK>

A;Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GB

R;Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; Mizobu-

submitted to the EMBL Data Library, December 1992

A;Description: Systematic sequencing of the Escherichia coli genome: analysis of the 0-2

A;Reference number: S40531

A;Accession: S40537

A;Molecule type: DNA

A;Residues: 1-376 <YUR>

A;Cross-references: EMBL:D10483; NID:g216434; PIDN:BAA01292.1; PID:g216441

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: G64721

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-376 <BLAT>

A;Cross-references: GB:AF000112; GB:U00096; NID:g1786192; PIDN:AAC73126.1; PID:g1786197;

A;Experimental source: strain K-12, substrain MG1655

C;Comment: This protein is induced by heat shock under the control of the htpR gene prod

C;Genetics:

A;Gene: dnaJ

A;Map position: 0 min

C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

C;Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein

F;5-70/Domain: dnaJ amino-terminal homology <DNJ>

F;77-106/Region: G/F motif

F;144-151/Region: CXXCXGXG repeat

F;161-168/Region: CXXCXGXG repeat

F;183-190/Region: CXXCXGXG repeat
F;197-204/Region: CXXCXGXG repeat

Query Match 100.0%; Score 86; DB 1; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 2

G90630 DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G90630
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HAY>
A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:BA000007; PIDN:BAB33438.1; PID:g1
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0015
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 3

G85481 chaperone with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, s
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85481
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85481
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <STO>
A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:AE005174; NID:g12512693; PIDN:AAG
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 4

AF0503

DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18),
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0503
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0503
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:g16501296; GSPDB:GN00176
C;Genetics:
A;Gene: STY0013
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 5

AB0058 chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0058
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, S
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <KUR>
A;Cross-references: UNIPROT:Q8ZIM6; GB:AL590842; PIDN:CAC89325.1; PID:g15978561; GSPDB:G
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||||
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 6

C64112 heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999
C;Accession: C64112
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64112
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-394 <TIGR>
A;Cross-references: GB:L42023; GB:U32803; NID:g1574162; PIDN:AAC22890.1; PID:g1574168; T
C;Genetics:
A;Gene: dnaJ
A;Start codon: GTG
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F;17-82/Domain: dnaJ amino-terminal homology <DNJ>
F;89-121/Region: G/F motif
F;159-166/Region: CXXCXGXG repeat
F;176-183/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat
F;212-219/Region: CXXCXGXG repeat

Query Match 100.0%; Score 86; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 73 QKRAAYDQYGHAAFEQ 88

RESULT 7
D82270
dnaJ protein VC0856 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82270
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-381 <HEI>
A;Cross-references: UNIPROT:O34242; GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF9401
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0856
A;Map position: 1
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 96.5%; Score 83; DB 2; Length 381;
Best Local Similarity 93.8%; Pred. No. 9.3e-07;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 8
S15295
nolC protein - Rhizobium fredii
C;Species: Rhizobium fredii
C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S15295
R;Krishnan, H.B.; Pueppke, S.G.
Mol. Microbiol. 5, 737-745, 1991
A;Title: nolC, a Rhizobium fredii gene involved in cultivar-specific nodulation of soybe
A;Reference number: S15295; MUID:91260457; PMID:1646377
A;Accession: S15295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <MOL>

A;Cross-references: UNIPROT:P26508; GB:L03521; NID:g152353; PIDN:AAA26333.1; PID:g152354
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 95.3%; Score 82; DB 2; Length 392;
Best Local Similarity 93.8%; Pred. No. 1.4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 60 QKRAAYDQYGHAAFEQ 75

RESULT 9
F84947
dnaJ protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F84947
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: F84947
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: dnaJ; BU152
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 87.2%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 2.3e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
: | | | | | | | | | | | | | | | |
Db 61 EKRSAAYDQYGHAAFE 75

RESULT 10
JC5609
heat shock protein dnaJ - Buchnera sp.
C;Species: Buchnera sp.
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: JC5609
R;Sato, S.; Ishikawa, H.
J. Biochem. 122, 41-48, 1997
A;Title: Structure and expression of the dnaKJ operon of Buchnera, an intracellular symb
A;Reference number: JC5608; MUID:97420684; PMID:9276669
A;Accession: JC5609
A;Molecule type: DNA
A;Residues: 1-377 <SAT>
A;Cross-references: DDBJ:D88673; NID:g2351215; PIDN:BAA21965.1; PID:g2351217
C;Comment: This protein binds to DnaK protein and GrpE protein and modulates the chaperon
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;5-70/Domain: dnaJ amino-terminal homology <DNJ>
F;77-108/Region: G/F motif
F;145-152/Region: CXXCXGXG repeat
F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGXG repeat

Query Match 87.2%; Score 75; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 2.3e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15

Db 61 EKRSAYDQYGHAAFE 75
:|||||
RESULT 11
D81242
DnaJ protein NMA0209 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004,
C;Accession: D81242; C82015
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81242
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <TET>
A;Cross-references: UNIPROT:P57107; GB:AE002366; GB:AE002098; NID:g7225284; PIDN:AAF4052
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: C82015
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-373 <PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83522.1; PID:g737897
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: dnaJ; NMB0059; NMA0209
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
Query Match 84.9%; Score 73; DB 2; Length 373;
Best Local Similarity 86.7%; Pred. No. 5.1e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
:|||||
Db 61 EKRAAYDQYGHAAFE 75
:|||||
RESULT 12
B47042
heat shock protein dnaJ - Brucella ovis
C;Species: Brucella ovis
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47042
R;Cellier, M.F.; Teyssier, J.; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri Widada, J.
J. Bacteriol. 174, 8036-8042, 1992
A;Title: Cloning and characterization of the Brucella ovis heat shock protein DnaK func
A;Reference number: A47042; MUID:93094135; PMID:1459952
A;Accession: B47042
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-375 <CEL>
A;Cross-references: UNIPROT:Q05980; EMBL:M95799; NID:gl44114; PIDN:AAC36133.1; PID:gl441
A;Note: sequence extracted from NCBI backbone (NCBIN:119966, NCBI:P:119968)
C;Genetics:
A;Gene: dnaJ
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C;Keywords: DNA replication; heat shock; molecular chaperone
F;4-69/Domain: dnaJ amino-terminal homology <DNJ>
F;76-108/Region: G/F motif
F;146-153/Region: CXXCXGXG repeat
F;163-170/Region: CXXCXGXG repeat
F;185-192/Region: CXXCXGXG repeat
F;199-206/Region: CXXCXGXG repeat

Query Match 84.9%; Score 73; DB 2; Length 375;
Best Local Similarity 86.7%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
:|||||
Db 60 QKRAAYDRFGHAAFE 74
:|||||
RESULT 13
D97373
Chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97373
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <KUR>
A;Cross-references: UNIPROT:P50018; GB:AE007869; PIDN:AAK85941.1; PID:g15154994; GSPDB:GN
C;Genetics:
A;Gene: AGR_C_192
A;Map position: circular chromosome
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
Query Match 84.9%; Score 73; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
:|||||
Db 61 QKRAAYDRFGHAAFE 75
:|||||
RESULT 14
AD2591
molecular chaperone, DnaJ family dnaJ [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2591
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <KUR>
A;Cross-references: UNIPROT:P50018; GB:AE008688; PIDN:AAL41146.1; PID:gl7738442; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dnaJ
A;Map position: circular chromosome
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
Query Match 84.9%; Score 73; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
:|||||
Db 61 QKRAAYDRFGHAAFE 75
:|||||

RESULT 15
AC3502
chaperone protein dnaJ [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3502
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Ietess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <KUR>
A;Cross-references: UNIPROT:Q8YE77; UNIPROT:Q8FXX1; GB:AE008917; PIDN:AAL53182.1; PID:gl
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI2001
A;Map position: 1
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 84.9%; Score 73; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. NO. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
||| ||| : ||| |||
Db 60 QKRAAYDRFGHAAFE 74

Search completed: March 7, 2005, 07:42:13
Job time : 10.1722 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:21:08 ; Search time 65.5894 Seconds
(without alignments)
124.918 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	372	Q7N8Y3	Q7n8y3 photorhabdu
2	86	100.0	375	1 DNAJ_ECOLI	P08622 escherichia
3	86	100.0	376	2 Q7UDU1	Q7udu1 shigella fl
4	86	100.0	376	2 Q8FLC5	Q8flc5 escherichia
5	86	100.0	376	2 Q8XA65	Q8xa65 escherichia
6	86	100.0	377	1 DNAJ_HAEDU	P48208 haemophilus
7	86	100.0	378	1 DNAJ_SALTY	Q60004 salmonella
8	86	100.0	379	2 Q8L3D3	Q8l3d3 colwellia m
9	86	100.0	379	2 Q66ES9	Q66es9 yersinia ps
10	86	100.0	379	2 Q8ZIM6	Q8zim6 yersinia pe
11	86	100.0	379	2 Q6D0B8	Q6d0b8 erwinia car
12	86	100.0	382	1 DNAJ_HAEIN	P43735 haemophilus
13	86	100.0	386	2 Q83MH4	Q83mh4 shigella fl
14	83	96.5	375	1 DNAJ_ACTAC	P77866 actinobacil
15	83	96.5	380	2 Q6LUA6	Q6lua6 photobacter
16	83	96.5	381	1 DNAJ_VIBCH	O34242 vibrio chol
17	83	96.5	381	2 Q87RX2	Q87rx2 vibrio para
18	83	96.5	381	2 Q8DF67	Q8df67 vibrio vuln
19	83	96.5	385	1 DNAJ_VIBHA	O87385 vibrio harv
20	83	96.5	386	2 Q7MN84	Q7mn84 vibrio vuln
21	83	96.5	389	2 Q65U54	Q65u54 mannheimia
22	82	95.3	379	2 Q92T07	Q92t07 rhizobium m
23	82	95.3	392	1 NOLC_RHIFR	P26508 rhizobium f
24	81	94.2	379	2 Q75WD2	Q75wd2 acetobacter
25	80	93.0	372	1 DNAJ_PASMU	Q9cms2 pasteurella
26	78	90.7	376	2 Q98DD2	Q98dd2 rhizobium l
27	77	89.5	234	1 DNAJ_RHILE	O3529 rhizobium l
28	77	89.5	331	2 Q93S23	Q93s23 rhizobium t
29	77	89.5	379	1 DNAJ_RHOPA	Q6ncy3 rhodopseudo
30	77	89.5	379	1 DNAJ_RHOS7	O08356 rhodopseudo
31	77	89.5	384	2 Q8RB67	Q8rb67 thermoanaer

32	75	87.2	377	1 DNAJ_BUCAI	O32465 buchnera ap
33	75	87.2	377	2 Q7VQC3	Q7vql3 candidatus
34	75	87.2	379	1 DNAJ_PASHA	O52065 pasteurella
35	75	87.2	383	1 DNAJ_BUCBP	Q89au7 buchnera ap
36	74	86.0	378	1 DNAJ_BUCAP	Q8k9y9 buchnera ap
37	73	84.9	370	1 DNAJ_ERYRH	Q05646 erysipeloth
38	73	84.9	373	1 DNAJ_NEIMA	P63968 neisseria m
39	73	84.9	373	1 DNAJ_NEIMB	P63969 neisseria m
40	73	84.9	375	1 DNAJ_BRUOV	Q05980 brucella ov
41	73	84.9	377	1 DNAJ_AGR5	P50018 agrobacteri
42	73	84.9	377	1 DNAJ_BRAJA	P94319 bradyrhizob
43	73	84.9	377	1 DNAJ_BRUME	Q8ye77 brucella me
44	73	84.9	377	1 DNAJ_BRUSU	Q8fxx1 brucella su
45	73	84.9	379	2 Q6RSN5	Q6rsn5 agrobacteri

ALIGNMENTS

RESULT 1

Q7N8Y3					
ID	Q7N8Y3	PRELIMINARY;	PRT;	372 AA.	
AC	Q7N8Y3;				
DT	01-MAR-2004 (TrEMBLrel. 26, Created)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	Heat shock protein dnaJ (HSP40) (Chaperone protein).				
GN	Name=dnaJ; OrderedLocusNames=plu0580;				
OS	Photorhabdus luminescens (subsp. laumondii).				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Photorhabdus.				
OX	NCBI_TaxID=141679;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TT01;				
RX	MEDLINE=22957627; PubMed=14528314;				
RA	Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,				
RA	Tacourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,				
RA	Dassa E., Deroose R., Derzelle S., Freyssinet G., Gaudriault S.,				
RA	Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,				
RA	Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.,				
RT	"The genome sequence of the entomopathogenic bacterium Photorhabdus				
RT	luminescens.";				
RL	Nat. Biotechnol. 21:1307-1313(2003).				
CC	-I- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,				
CC	the ATPase activity of dnaK (By similarity).				
CC	-I- COFACTOR: Binds 2 zinc ions per monomer (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).				
CC	-I- SIMILARITY: Belongs to the dnaJ family.				
DR	EMBL; BX571860; CAB12875.1; -.				
DR	HSSP; P08622; 1BQZ.				
DR	PhotoList; plu0580; -.				
DR	GO; GO:0051082; F:unfolded protein binding; IEA.				
DR	GO; GO:0006260; P:DNA replication; IEA.				
DR	GO; GO:0006457; P:protein folding; IEA.				
DR	GO; GO:0006986; P:response to unfolded protein; IEA.				
DR	InterPro; IPR000345; CytC_heme_BS.				
DR	InterPro; IPR002939; DnaJ_C.				
DR	InterPro; IPR001305; DnaJ_CXXCXGXG.				
DR	InterPro; IPR001623; DnaJ_N.				
DR	InterPro; IPR008971; HSP40_DnaJ_pep.				
DR	InterPro; IPR003095; Hsp_DnaJ.				
DR	Pfam; PF00226; DnaJ; 1.				
DR	Pfam; PF01556; DnaJ_C; 1.				
DR	Pfam; PF00684; DnaJ_CXXCXGXG; 1.				
DR	PRINTS; PR00625; DNAJPROTEIN.				
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.				
DR	PROSITE; PS00636; DNAJ_1; 1.				
DR	PROSITE; PS50076; DNAJ_2; 1.				
DR	PROSITE; PS00637; DNAJ_CXXCXGXG; 1.				
KW	Chaperone; Complete proteome; DNA replication; Heat shock;				
KW	Metal-binding; Repeat; Zinc.				
SQ	SEQUENCE 372 AA; 40820 MW; B2F36918CC6E9B1A CRC64;				

Query Match 100.0%; Score 86; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 2
DNAJ_ECOLI STANDARD; PRT; 375 AA.
AC P08622;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Chaperone protein dnaJ (Heat shock protein J) (HSP40).
GN Name=dnaJ; Synonyms=groP; OrderedLocusNames=b0015;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RX MEDLINE=86111849; PubMed=3003084;
RA Ohki M., Tamura F., Nishimura S., Uchida H.;
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and
RT purification of the gene product.";
RL J. Biol. Chem. 261:1778-1781(1986).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=86111850; PubMed=3003085;
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M.,
RA Georgopoulos C.;
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene. A
RT gene that encodes a heat shock protein.";
RL J. Biol. Chem. 261:1782-1785(1986).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92334977; PubMed=1630901;
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RA Isono K., Mizobuchi K., Nakata A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [4]

RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]

RP POSSIBLE FUNCTION.
RX MEDLINE=91187894; PubMed=1826368;
RA Liberek K., Marszalek J., Ang D., Georgopoulos C., Zylicz M.;
RT "Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate
RT ATPase activity of DnaK.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
RN [6]

RP STRUCTURE BY NMR OF 1-107.
RX MEDLINE=96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
RA Pellechia M., Szyperski T., Wali D., Georgopoulos C., Wuthrich K.;
RT "NMR structure of the J-domain and the Gly/Phe-rich region of the
RT Escherichia coli DnaJ chaperone.";
RL J. Mol. Biol. 260:236-250(1996).
RN [7]

RP STRUCTURE BY NMR OF 1-104.
RX MEDLINE=99224904; PubMed=10210198;
RA Huang K., Flanagan J.M., Prestegard J.H.;
RT "The influence of C-terminal extension on the structure of the 'J'-
RT domain' in E. coli DnaJ.";
RL Protein Sci. 8:203-214(1999).
RN [8]
RP STRUCTURE BY NMR OF 130-208.
RX MEDLINE=20351465; PubMed=10891270; DOI=10.1006/jmbi.2000.3923;
RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
RT "Solution structure of the cysteine-rich domain of the Escherichia
RT coli chaperone protein DnaJ.";
RL J. Mol. Biol. 300:805-818(2000).
CC -!- FUNCTION: Interacts with dnaK to disassemble a protein complex at
CC the phage lambda origin of replication. Stimulates, jointly with
CC grpE, the ATPase activity of dnaK.
CC -!- COFACTOR: Binds 2 zinc ions per monomer.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: By heat shock under the control of the htpR regulatory
CC protein.
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M12544; AAA00009.1; -.
DR EMBL; M12565; AAA23693.1; -.
DR EMBL; D10483; BAB96590.1; -.
DR EMBL; U00096; AAC73126.1; -.
DR PIR; A92572; HHECDJ.
DR PDB; 1BQ0; NMR; @=1-103.
DR PDB; 1BQ2; NMR; @=1-77.
DR PDB; 1EXK; NMR; A=130-208.
DR PDB; 1XBL; NMR; @=1-107.
DR ECO2DBASE; H036.5; 6TH EDITION.
DR EchoBASE; EB0236; -.
DR EcoGene; EG10240; dnaJ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pep.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW 3D-structure; Chaperone; Complete proteome; Direct protein sequencing;
KW DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
FT INIT MET 0 0 J-domain.
FT DOMAIN 2 71 Gly-rich.
FT DOMAIN 76 113 CXXCXGKG motif.
FT REPEAT 143 150 CXXCXGKG motif.
FT REPEAT 160 167 CXXCXGKG motif.
FT REPEAT 182 189 CXXCXGKG motif.
FT REPEAT 196 203 CXXCXGKG motif.
FT METAL 143 143 Zinc 1.
FT METAL 146 146 Zinc 1.
FT METAL 160 160 Zinc 2.
FT METAL 163 163 Zinc 2.
FT METAL 182 182 Zinc 2.

FT METAL 185 185 Zinc 2.
FT METAL 196 196 Zinc 1.
FT METAL 199 199 Zinc 1.
FT HELIX 5 8
FT TURN 9 10
FT TURN 13 14
FT HELIX 18 31
FT TURN 32 35
FT HELIX 36 38
FT TURN 41 42
FT HELIX 43 50
FT TURN 51 51
FT HELIX 52 56
FT HELIX 59 64
FT HELIX 65 67
FT TURN 68 73
FT TURN 131 133
FT STRAND 140 142
FT HELIX 144 146
FT TURN 147 149
FT STRAND 151 151
FT STRAND 158 159
FT TURN 161 165
FT STRAND 168 173
FT TURN 174 175
FT STRAND 176 181
FT TURN 183 187
FT STRAND 190 191
FT STRAND 195 195
FT HELIX 197 199
FT TURN 200 201
FT STRAND 204 206
SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0BD8C3F CRC64;

Query Match 100.0%; Score 86; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFEQ 16
|||||
Db 60 OKRAAYDOYGHAAFEQ 75

RESULT 3
Q7UDU1 PRELIMINARY; PRT; 376 AA.
AC Q7UDU1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone with DnaK; heat shock protein.
GN Name=dnaJ; OrderedLocusNames=S0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2457T;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE016978; AAP15561.1; -.
DR HSSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS00076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Heat shock.
SQ SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDOYGHAAFEQ 16
|||||
Db 61 OKRAAYDOYGHAAFEQ 76

RESULT 4
Q8FLC5 PRELIMINARY; PRT; 376 AA.
AC Q8FLC5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=c0020;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE016755; AAN78520.1; -.
DR PIR; G85481; G85481.
DR PIR; G90630; G90630.
DR HSSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

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DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 5
Q8XA65 PRELIMINARY; PRT; 376 AA.
AC Q8XA65; Q7AHU4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone with DnaK; heat shock protein (DnaJ protein).
GN Name=dnaJ; OrderedLocusNames=ECs0015, z0015;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL; AE005178; AAG54315.1; -.
DR EMBL; AP002550; BAB33438.1; -.
DR PIR; G85481; G85481.
DR PIR; G90630; G90630.
DR HSSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.
DR PRINTS; PS00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc;
KW Complete proteome.
SQ SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;

Query Match 100.0%; Score 86; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 6
DnaJ_HAEDU STANDARD; PRT; 377 AA.
AC P48208;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=HD0188;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Parsons L.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
DR EMBL; U25996; AAA67299.1; -.
DR EMBL; AE017151; AAP95181.1; -.
DR HSSP; P08622; 1BQZ.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGKG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
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DR	Pfam; PF00684; DnaJ_CXXCXGKG; 1.	RA	Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
DR	PRINTS; PR00625; DNAJPROTEIN.	RA	Whitehead S., Barrell B.G.;
DR	PROSITE; PS00636; DnaJ_1; 1.	RT	"Complete genome sequence of a multiple drug resistant Salmonella
DR	PROSITE; PS50076; DnaJ_2; 1.	RT	enterica serovar Typhi CT18.";
DR	PROSITE; PS00637; DnaJ_CXXCXGKG; 1.	RL	Nature 413:848-852(2001).
KW	Chaperone; Complete proteome; DNA replication; Heat shock;	RN	[4]
KW	Metal-binding; Repeat; Zinc.	RP	SEQUENCE FROM N.A.
FT	DOMAIN 3 72 J-domain.	RC	SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
FT	DOMAIN 77 108 Gly-rich.	RX	MEDLINE=22531367; PubMed=12644504;
FT	REPEAT 147 154 CXXCXGKG motif.	RX	DOI=10.1128/JB.185.7.2330-2337.2003;
FT	REPEAT 164 171 CXXCXGKG motif.	RA	Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
FT	REPEAT 186 193 CXXCXGKG motif.	RA	Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
FT	REPEAT 200 207 CXXCXGKG motif.	RT	"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
FT	METAL 147 147 Zinc 1 (By similarity).	RT	and CT18.";
FT	METAL 150 150 Zinc 1 (By similarity).	RL	J. Bacteriol. 185:2330-2337(2003).
FT	METAL 164 164 Zinc 2 (By similarity).	CC	- - FUNCTION: Interacts with dnaK to disassemble a protein complex at
FT	METAL 167 167 Zinc 2 (By similarity).	CC	the phage lambda origin of replication. Stimulates, jointly with
FT	METAL 186 186 Zinc 2 (By similarity).	CC	grpE, the ATPase activity of dnaK.
FT	METAL 189 189 Zinc 2 (By similarity).	CC	- - COFACTOR: Binds 2 zinc ions per monomer (By similarity).
FT	METAL 200 200 Zinc 2 (By similarity).	CC	- - SUBUNIT: Homodimer (By similarity).
FT	METAL 203 203 Zinc 1 (By similarity).	CC	- - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SQ	SEQUENCE 377 AA; 41027 MW; 37E9048F81A1A7A9 CRC64;	CC	- - INDUCTION: By heat shock under the control of the htpR regulatory
		CC	protein (By similarity).
		CC	- - SIMILARITY: Belongs to the dnaJ family.
		CC	- - SIMILARITY: Contains 1 CR domain.
		CC	- - SIMILARITY: Contains 1 J domain.
		CC	-----
Qy	1 QKRAAYDQYGHAAFEQ 16	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
		CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	61 QKRAAYDQYGHAAFEQ 76	CC	the European Bioinformatics Institute. There are no restrictions on its
		CC	use by non-profit institutions as long as its content is in no way
		CC	modified and this statement is not removed. Usage by and for commercial
		CC	entities requires a license agreement (See http://www.isb-sib.ch/
		CC	or send an email to license@isb-sib.ch).
		CC	-----
RESULT 7		CC	EMBL; U58360; AAB02911.1; --
DNAJ_SALTY		DR	EMBL; AE008693; AAL18977.1; --
ID_DNAJ_SALTY STANDARD; PRT; 378 AA.		DR	EMBL; AL627265; CAD01166.1; --
AC Q60004;		DR	EMBL; AE016834; AAO67747.1; --
DT 01-NOV-1997 (Rel. 35, Created)		DR	HSSP; P08622; 1EXK.
DT 15-DEC-1998 (Rel. 37, Last sequence update)		DR	StyGene; SG10620; dnaJ.
DT 25-OCT-2004 (Rel. 45, Last annotation update)		DR	InterPro; IPR002939; DnaJ_C.
DE Chaperone protein dnaJ.		DR	InterPro; IPR001305; DnaJ_CXXCXGKG.
GN Name=dnaJ; OrderedLocusNames=STM0013, STY0013, t0013;		DR	InterPro; IPR001623; DnaJ_N.
OS Salmonella typhimurium, and		DR	InterPro; IPR008971; HSP40_DnaJ_pap.
OS Salmonella typhi.		DR	InterPro; IPR003095; Hsp DnaJ.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		DR	InterPro; IPR011031; Multihaem_cyt.
OC Enterobacteriaceae; Salmonella.		DR	Pfam; PF00226; DnaJ; 1.
OX NCBI_TaxID=602, 601;		DR	Pfam; PF01556; DnaJ_C; 1.
RN [1]		DR	Pfam; PF00684; DnaJ_CXXCXGKG; 1.
RP SEQUENCE FROM N.A.		DR	PRINTS; PR00625; DNAJPROTEIN.
RC SPECIES=S.typhimurium; STRAIN=LT2;		DR	SMART; SM00271; DnaJ; 1.
Stephen R.J., Hinton J.C.D.;		DR	PROSITE; PS00636; DnaJ_1; 1.
Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.		DR	PROSITE; PS50076; DnaJ_2; 1.
[2]		DR	PROSITE; PS00637; DnaJ_CXXCXGKG; 1.
SEQUENCE FROM N.A.		KW	Chaperone; Complete proteome; DNA replication; Heat shock;
SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;		KW	Metal-binding; Repeat; Zinc.
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;		FT	INIT_MET 0 0 By similarity.
McClelland M., Sanderson K.E., Slieth J., Clifton S.W., Latreille P.,		FT	DOMAIN 2 71 J-domain.
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,		FT	DOMAIN 76 112 Gly-rich.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,		FT	REPEAT 146 153 CXXCXGKG motif.
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,		FT	REPEAT 163 170 CXXCXGKG motif.
Waterston R., Wilson R.K.;		FT	REPEAT 185 192 CXXCXGKG motif.
"Complete genome sequence of Salmonella enterica serovar Typhimurium		FT	REPEAT 199 206 CXXCXGKG motif.
LT2.";		FT	METAL 146 146 Zinc 1 (By similarity).
Nature 413:852-856(2001).		FT	METAL 149 149 Zinc 1 (By similarity).
[3]		FT	METAL 163 163 Zinc 2 (By similarity).
SEQUENCE FROM N.A.		FT	METAL 166 166 Zinc 2 (By similarity).
SPECIES=S.typhi; STRAIN=CT18;		FT	METAL 185 185 Zinc 2 (By similarity).
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;		FT	METAL 188 188 Zinc 2 (By similarity).
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,		FT	METAL 199 199 Zinc 1 (By similarity).
Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,		FT	METAL 202 202 Zinc 1 (By similarity).
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,		SQ	SEQUENCE 378 AA; 41181 MW; 176EEC64696F30A2 CRC64;
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,			
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,			

Query Match 100.0%; Score 86; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 60 QKRAAYDQYGHAAFEQ 75

RESULT 8

Q8L3D3 PRELIMINARY; PRT; 379 AA.
AC Q8L3D3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 40.
GN Name=dnaJ;
OS Colwellia maris (Vibrio sp. (strain ABE-1)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Colwelliaceae; Colwellia.
OX NCBI_TaxID=77524;
RN [1]

SEQUENCE FROM N.A.

RA Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084455; BAB91324.2; -.
DR HSSP; P08622; 1BQZ.

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pep.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

DR PROSITE; PS00636; DnaJ_1; 1.

DR PROSITE; PS00076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

KW Heat shock.

SQ SEQUENCE 379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;

Query Match

Best Local Similarity 100.0%; Score 86; DB 2; Length 379;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 9

Q66ES9 PRELIMINARY; PRT; 379 AA.
ID Q66ES9
AC Q66ES9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein, DnaJ and GrpE stimulates ATPase activity of DnaK.
DE DnaK.
GN Name=dnaJ; Synonyms=grpC; ORFNames=YPTB0612;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;
RN [1]

SEQUENCE FROM N.A.

RP

RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; BX936398; CAH19852.1; -.

DR GO; GO:0006457; P:protein folding; IEA.

DR GO; GO:0006986; P:response to unfolded protein; IEA.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGKG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pep.

DR InterPro; IPR003095; Hsp_DnaJ.

DR InterPro; IPR011031; Multihaem_cyt.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGKG; 1.

DR PRINTS; PR00625; DnaJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00636; DnaJ_1; 1.

DR PROSITE; PS00076; DnaJ_2; 1.

DR PROSITE; PS00637; DnaJ_CXXCXGKG; 1.

KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.

SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match

Best Local Similarity 100.0%; Score 86; DB 2; Length 379;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 10

Q8ZIM6 PRELIMINARY; PRT; 379 AA.
ID Q8ZIM6
AC Q8ZIM6; Q74Q12; Q7CG76;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone protein DnaJ (Chaperone with DnaK; heat shock protein).
GN Name=dnaJ; Synonyms=dnaJ2, grpC;
OrderedLocusNames=Yp3711, Yp00469, Y3705;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]

SEQUENCE FROM N.A.

RP

RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL: AJ414142; AAC89325.1; -.
DR EMBL: AE013974; AAC87253.1; -.
DR EMBL: AE017141; AAS63859.1; -.
DR PIR: AB0058; AB0058.
DR HSSP: P08622; 1EXK.
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR GO: GO:0006986; P:response to unfolded protein; IEA.
DR Pfam: PF00226; DnaJ; 1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS: PR00625; DNAJPROTEIN.
DR SMART: SM00271; DnaJ; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 41278 MW; AC1922FC3D707C93 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
|||||

RESULT 11
Q6D0B8 ID Q6D0B8 PRELIMINARY; PRT; 379 AA.
AC Q6D0B8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chaperone protein DnaJ.
GN Name=dnaJ; OrderedLocusNames=ECA3881;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,

RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
DR EMBL: BX950851; CAG76779.1; -.
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR000345; CytC_heme_BS.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXGXG.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR008971; HSP40_DnaJ_pdp.
DR InterPro: IPR003095; Hsp_DnaJ.
DR InterPro: IPR011031; Multihaem_cyt.
DR Pfam: PF00226; DnaJ; 1.
DR Pfam: PF01556; DnaJ_C; 1.
DR Pfam: PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS: PR00625; DNAJPROTEIN.
DR SMART: SM00271; DnaJ; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS50076; DnaJ_2; 1.
DR PROSITE: PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
|||||

RESULT 12
DNAJ_HAEIN ID DNAJ_HAEIN STANDARD; PRT; 382 AA.
AC P43735;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ; OrderedLocusNames=HI1238;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC -!- SIMILARITY: Contains 1 CR domain.
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
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CC -----
DR EMBL; U32803; AAC22890.1; ALT_INIT.
DR HSSP; P08622; IBQZ.
DR TIGR; H11238; -.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR InterPro; IPR011031; Multihaem_cyt.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
FT DOMAIN 3 72 J-domain.
FT DOMAIN 77 110 Gly-rich.
FT REPEAT 147 154 CXXCXGXG motif.
FT REPEAT 164 171 CXXCXGXG motif.
FT REPEAT 186 193 CXXCXGXG motif.
FT REPEAT 200 207 CXXCXGXG motif.
FT METAL 147 147 Zinc 1 (By similarity).
FT METAL 150 150 Zinc 1 (By similarity).
FT METAL 164 164 Zinc 2 (By similarity).
FT METAL 167 167 Zinc 2 (By similarity).
FT METAL 186 186 Zinc 2 (By similarity).
FT METAL 189 189 Zinc 2 (By similarity).
FT METAL 200 200 Zinc 1 (By similarity).
FT METAL 203 203 Zinc 1 (By similarity).
SQ SEQUENCE 382 AA; 41222 MW; 8850B88B6FB2BC2B CRC64;

Query Match 100.0%; Score 86; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 13
Q83MH4 PRELIMINARY; PRT; 386 AA.
AC Q83MH4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chaperone with DnaK; heat shock protein.
GN Name=dnaJ; OrderedLocusNames=SF0015;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
CC the ATPase activity of dnaK (By similarity).
CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the dnaJ family.
CC EMBL; AE015039; AAN41681.1; -.
DR HSSP; P08622; 1EXK.
DR GO; GO:0051082; F:unfolded protein binding; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR002939; DnaJ_C.
DR InterPro; IPR001305; DnaJ_CXXCXGXG.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR008971; HSP40_DnaJ_pap.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF01556; DnaJ_C; 1.
DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.
DR PRINTS; PR00625; DnaJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
DR PROSITE; PS00636; DnaJ_1; 1.
DR PROSITE; PS50076; DnaJ_2; 1.
DR PROSITE; PS00637; DnaJ_CXXCXGXG; 1.
KW Chaperone; Complete proteome; DNA replication; Heat shock;
KW Metal-binding; Repeat; Zinc.
SQ SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;

Query Match 100.0%; Score 86; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 71 QKRAAYDQYGHAAFEQ 86

RESULT 14
DnaJ_ACTAC STANDARD; PRT; 375 AA.
ID DnaJ ACTAC
AC P77866;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chaperone protein dnaJ.
GN Name=dnaJ;
OS Actinobacillus actinomycetemcomitans (Haemophilus
OS actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y4;
RX MEDLINE=98182595; PubMed=9522128;
RA Yoshida A., Nakano Y., Yamashita Y., Yu H., Ohishi M., Koga T.;
RT "Isolation and characterization of the dnaK operon from
RT Actinobacillus actinomycetemcomitans.";
RL DNA Seq. 8:93-98(1997).
RN -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

CC the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

CC -!- SIMILARITY: Contains 1 CR domain.

CC -!- SIMILARITY: Contains 1 J domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; D87753; BAA32697.1; --

DR HSSP; P08622; 1BQZ.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGXG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pep.

DR InterPro; IPR003095; Hsp_DnaJ.

DR InterPro; IPR011031; Multihaem_cyt.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.

DR PRINTS; PR00625; DNAJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00636; DNAJ_1; 1.

DR PROSITE; PS50076; DNAJ_2; 1.

DR PROSITE; PS00637; DNAJ_CXXCXGXG; 1.

KW Chaperone; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.

FT DOMAIN 5 70

FT REPEAT 77 110 Gly-rich.

FT REPEAT 145 152 CXXCXGXG motif.

FT REPEAT 162 169 CXXCXGXG motif.

FT REPEAT 184 191 CXXCXGXG motif.

FT REPEAT 198 205 CXXCXGXG motif.

FT METAL 145 145 Zinc 1 (By similarity).

FT METAL 148 148 Zinc 1 (By similarity).

FT METAL 162 162 Zinc 2 (By similarity).

FT METAL 165 165 Zinc 2 (By similarity).

FT METAL 184 184 Zinc 2 (By similarity).

FT METAL 187 187 Zinc 2 (By similarity).

FT METAL 198 198 Zinc 1 (By similarity).

FT METAL 201 201 Zinc 1 (By similarity).

SQ SEQUENCE 375 AA; 41374 MW; CF9D286756FF44E1 CRC64;

Query Match 96.5%; Score 83; DB 1; Length 375;
Best Local Similarity 93.8%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 EKRAAYDQYGHAAFEQ 76

RESULT 15

Q6LUA6

ID Q6LUA6 PRELIMINARY; PRT; 380 AA.

AC Q6LUA6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Putative DnaJ protein; DnaJ-class molecular chaperone with C-terminal

DE Zn finger domain.

GN Name=ECS0015; OrderedLocusNames=PBPA0698;

OS Photobacterium profundum (Photobacterium sp. (strain SS9)).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Photobacterium.

OX NCBI_TaxID=74109;

RN [1]

RP SEQUENCE FROM N.A.

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,

RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,

RA Valle G.;

RT "Genome analysis of Photobacterium profundum reveals the complexity of

RT high pressure adaptations.";

RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.

CC -!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

CC the ATPase activity of dnaK (By similarity).

CC -!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the dnaJ family.

DR EMBL; CR378665; CAG19119.1; --

DR GO; GO:0051082; F:unfolded protein binding; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR000345; CytC_heme_BS.

DR InterPro; IPR002939; DnaJ_C.

DR InterPro; IPR001305; DnaJ_CXXCXGXG.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR008971; HSP40_DnaJ_pep.

DR InterPro; IPR003095; Hsp_DnaJ.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF01556; DnaJ_C; 1.

DR Pfam; PF00684; DnaJ_CXXCXGXG; 1.

DR PRINTS; PR00625; DNAJPROTEIN.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.

DR PROSITE; PS00636; DNAJ_1; 1.

DR PROSITE; PS50076; DNAJ_2; 1.

DR PROSITE; PS00637; DNAJ_CXXCXGXG; 1.

KW Chaperone; Complete proteome; DNA replication; Heat shock;

KW Metal-binding; Repeat; Zinc.

SQ SEQUENCE 380 AA; 40802 MW; 772DD9F069899B63 CRC64;

Query Match 96.5%; Score 83; DB 2; Length 380;
Best Local Similarity 93.8%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 60 QKRAAYDQYGHAAFEQ 75

Search completed: March 7, 2005, 07:52:39
Job time : 67.5894 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:13:17 ; Search time 77.9868 Seconds
(without alignments)
79.349 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5	AAU98852
2	86	100.0	16	6	ABR55126
3	86	100.0	131	3	AAB11396
4	86	100.0	131	4	AAB74197
5	86	100.0	131	4	AAB70767
6	86	100.0	131	4	AAY72018
7	86	100.0	340	4	AAU17588
8	86	100.0	340	7	ADB94296
9	86	100.0	341	4	AAU17587
10	86	100.0	341	7	ADB94295
11	86	100.0	373	6	ABM67485
12	86	100.0	376	8	ADR89339
13	86	100.0	376	8	ADN18036
14	86	100.0	378	8	ADN17733
15	86	100.0	378	8	ADS42875
16	86	100.0	380	7	ADF05627
17	86	100.0	380	7	ABO62494
18	86	100.0	399	3	AAB11395
19	86	100.0	399	4	AAB74196
20	86	100.0	399	4	AAB70766
21	86	100.0	399	4	AAY72017
22	86	100.0	476	4	ABG17771
23	81	94.2	15	2	AAW25795
24	81	94.2	15	3	AAY79543
25	81	94.2	15	4	AAM99341

26	81	94.2	15	5	AAU09842
27	81	94.2	15	5	AAU98876
28	81	94.2	15	5	AAE19457
29	81	94.2	15	6	ABR55132
30	81	94.2	16	4	AAM99344
31	81	94.2	118	4	AAU02075
32	81	94.2	459	4	AAU02077
33	79	91.9	365	8	ADS21615
34	78	90.7	376	8	ADS23054
35	73	84.9	344	6	ABP80877
36	72	83.7	15	2	AAR95446
37	72	83.7	15	2	AAW25796
38	72	83.7	15	5	AAE19458
39	72	83.7	15	6	ABR55133
40	69	80.2	382	8	ADN25412
41	69	80.2	384	8	ADS43419
42	67	77.9	376	8	ADR31368
43	67	77.9	379	8	ADN24677
44	67	77.9	380	8	ADN21920
45	64.5	75.0	14	2	AAR95445

ALIGNMENTS

RESULT 1:
AAU98852
ID AAU98852 standard; peptide; 16 AA.

XX AAU98852;
AC
XX
DT 22-AUG-2002 (first entry)
XX
DE
DE E.Coli DNAJ 61 immunogenic peptide.
XX

KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytosstatic; antiinflammatory; antibacterial; antiarthritic;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer;
KW mucosal tolerisation; DNA vaccination; anergy induction.

XX Escherichia coli.

XX WO200236611-A2.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-US045344.

XX 01-NOV-2000; 2000US-0245181P.

XX (REGC) UNIV CALIFORNIA.

XX (MART/) MARTINI A.

XX Martini A, Albani S, Carson DA, Prakken BJ;

XX WPI; 2002-489999/52.

XX New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.

XX Claim 4; Page 55; 84pp; English.

XX This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating (i.e. augmenting/inducing or reducing/inhibiting) an immune response in a subject having an

CC immunological disorder (e.g. autoimmune disease such as arthritis or
CC articular juvenile idiopathic arthritis), an infectious disease, an
CC inflammatory bowel disease or cancer. The immunogenic peptide of the
CC invention is also useful for modulating immunoeffector cell
CC responsiveness in a subject. The immunogenic peptide is particularly
CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
CC general, the peptide is useful in methods involving mucosal tolerisation,
CC DNA vaccination, anergy induction or active immunisation. The present
CC sequence represents an E. coli DNAJ immunogenic peptide of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
ABR55126
ID ABR55126 standard; peptide; 16 AA.
XX
AC ABR55126;
XX
DT 03-JUL-2003 (first entry)
XX
DE E. coli dnaJ61 antigen-specific epitope peptide.
XX
KW Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytostatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW antiallergic; dermatological; antipsoriatic.
XX
OS Escherichia coli.
XX
PN WO2003026579-A2.
XX
PD 03-APR-2003.
XX
PF 25-SEP-2002; 2002WO-US030578.
XX
PR 25-SEP-2001; 2001US-0325499P.
PR 11-DEC-2001; 2001US-0339284P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Albani S, Martins A;
XX
DR WPI; 2003-430097/40.
XX
PT Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.
XX
PS Disclosure; Page 9; 41pp; English.
XX

The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the

CC invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 3
AAB11396
ID AAB11396 standard; protein; 131 AA.
XX
AC AAB11396;
XX
DT 22-FEB-2001 (first entry)
XX
DE E. coli expression plasmid PUBS520-pIN-J-Domain encoded protein.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
KW disulfide bridge.
XX
OS Escherichia coli.
OS Synthetic.
XX
PN EP1048732-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-1999; 99EP-00107412.
XX
PR 26-APR-1999; 99EP-00107412.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
DR WPI; 2000-674185/66.
DR N-PSDB; AAC66072.
XX
PT Preparation of water-soluble eukaryotic polypeptides with disulfide
PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT presence of arginine or amide compound.
XX
PS Example 3; Page 17; 40pp; German.
XX

This invention describes a novel preparation of a water-soluble,
CC naturally occurring eukaryotic polypeptide containing two or more
CC cysteine units bound via a disulfide bridge which comprises cultivation
CC of prokaryotic cells in the presence of arginine or an amide compound.
CC The method is useful for the preparation of eukaryotic proteins e.g.
CC proteases, interferons, protein hormones, antibodies or antibody
CC fragments (e.g. a single chain FV fragment that binds to thyroid
CC stimulating hormone). It is especially useful for preparing proteins with
CC more than five disulfide bridges, e.g. recombinant plasminogen activator
CC (rPA). The technique is simple and does not require in vitro after-
CC treatment, such as the removal of inclusion bodies, reduction or
CC naturization
XX

Sequence 131 AA;

Query Match 100.0%; Score 86; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 4

PR 02-OCT-2000; 2000US-02337039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-02399335P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249209P.
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PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDE; AAS27505.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX

PS Claim 1; SEQ ID NO 1153; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders (e.g. Addison's
CC epithelial cell proliferation, endocrine disorders, in wound healing,
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid
CC sequences of the invention
XX

Query Match 100.0%; Score 86; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
Db 25 QKRAAYDQYGHAAFEQ 40
|||||

RESULT 8

ADB94296
ID ADB94296 standard; protein; 340 AA.

XX ADB94296;

XX 04-DEC-2003 (first entry)

DE Human novel protein #530.

XX human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.

OS Homo sapiens.

XX US2002168711-A1.

XX 14-NOV-2002.

XX 17-JAN-2001; 2001US-00764868.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 17-NOV-2000; 2000US-0249299P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-719985/68.
N-PSDB; ADB93673.

New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's disease.

Claim 11; SEQ ID NO 1153; 345pp; English.

The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide. The polypeptide is also useful for identifying a binding partner to the polypeptide, which involves contacting the polypeptide with a binding partner and determining whether the binding partner effects an activity of the polypeptide. The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing, treating, or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the presence or absence of a mutation in the nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating autoimmune disease, Parkinson's disease, silicosis, gastrointestinal disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,

CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents the amino acid sequence of a novel human
CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format direct from
CC USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.

XX Sequence 340 AA;

Query Match 100.0%; Score 86; DB 7; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 25 QKRAAYDQYGHAAFEQ 40

RESULT 9

AAU17587

ID AAU17587 standard; protein; 341 AA.

XX AAU17587;

AC AAU17587;

XX 07-NOV-2001 (first entry)

DT Novel signal transduction pathway protein, Seq ID 1152.

DE Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;

XX antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;

KW immune system disorder; rheumatoid arthritis; inflammatory condition;

KW organ transplant rejection; infection; hepatitis C; blood disorder;

KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;

KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;

KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;

KW reproductive system; gastrointestinal; liver disorder; AIDS;

KW acquired immune deficiency syndrome.

XX Homo sapiens.

OS WO200154733-A1.

XX 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US001312.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

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PR 14-AUG-2000; 2000US-0224518P.

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PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
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PR 08-SEP-2000; 2000US-0231242P.
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PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
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PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 29-SEP-2000; 2000US-0236327P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 13-OCT-2000; 2000US-0239937P.
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PR 20-OCT-2000; 2000US-0241787P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
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PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
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PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
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PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
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PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
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PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27504.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders.
XX
PS Claim 1; SEQ ID NO 1152; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative disorders
CC (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), chromosomal abnormalities
CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),
CC respiratory disorders, dermatological disorders (e.g. wound healing,
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's
CC disease), reproductive system disorders, gastrointestinal disorder
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of
CC B-cell responsiveness to pathogens, activators of T-cells, to induce
CC higher affinity antibodies, and as a means to induce tumour proliferation
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-
CC AAU17683 represent novel signal transduction pathway protein, amino acid

```
CC sequences of the invention
XX
    Query Match      100.0%; Score 86; DB 4; Length 341;
    Best Local Similarity 100.0%; Pred. No. 1.3e-06;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 26 QKRAAYDQYGHAAFEQ 41

RESULT 10
ADB94295
ID ADB94295 standard; protein; 341 AA.
XX
AC ADB94295;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human novel protein #529.
XX
KW human; autoimmune disease; Parkinson's disease; silicosis;
KW gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia;
KW immunosuppressive agent; adjuvant; enhance immune response;
KW higher affinity antibody induction;
KW increased serum immunoglobulin concentration.
XX
OS Homo sapiens.
XX
XX US2002168711-A1.
XX
PD 14-NOV-2002.
XX
XX 17-JAN-2001; 2001US-00764868.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
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PR 14-AUG-2000; 2000US-0225267P.
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PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 22-AUG-2000; 2000US-0226868P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 27-SEP-2000; 2000US-0235834P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.

02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241809P.
01-NOV-2000; 2000US-0244617P.
17-NOV-2000; 2000US-0249299P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
XX
XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-719985/68.
DR N-PSDB; ADB93672.
XX
PT New isolated polypeptide useful for diagnosing and treating
PT immunosuppressive conditions such as autoimmune disease and Parkinson's
PT disease.
XX
PS Claim 11; SEQ ID NO 1152; 345pp; English.
XX
CC The invention relates to an isolated polypeptide. The polypeptide is
CC useful for diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject, by determining the presence or
CC amount of expression of the polypeptide in a biological sample and
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition based on the presence or amount of expression of the
CC polypeptide. The polypeptide is also useful for identifying a binding
CC partner to the polypeptide, which involves contacting the polypeptide
CC with a binding partner and determining whether the binding partner
CC effects an activity of the polypeptide. The polypeptide or the nucleic
CC acid encoding the polypeptide is useful for preventing, treating, or
CC ameliorating a medical condition, which involves administering the
CC polypeptide or the nucleic acid to a mammalian subject. The nucleic acid
CC is useful for diagnosing a pathological condition or a susceptibility to
CC a pathological condition in a subject, which involves determining the
CC presence or absence of a mutation in the nucleic acid, and diagnosing a
CC pathological condition or susceptibility to a pathological condition
CC based on the presence or absence of the mutation. The polypeptide, the
CC nucleic acid and an antibody to the polypeptide are useful for treating
CC autoimmune disease, Parkinson's disease, silicosis, gastrointestinal
CC disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide,
CC the nucleic acid and the antibody are useful as immunosuppressive agents,
CC as adjuvants to enhance immune responses, and as agents to induce higher
CC affinity antibodies and increase serum immunoglobulin concentrations. The
CC present sequence represents the amino acid sequence of a novel human
CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format direct from
CC USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
XX
SQ Sequence 341 AA;

    Query Match      100.0%; Score 86; DB 7; Length 341;
    Best Local Similarity 100.0%; Pred. No. 1.3e-06;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 26 QKRAAYDQYGHAAFEQ 41

RESULT 11
ABM67485
ID ABM67485 standard; protein; 373 AA.
XX
```


AC ABM67485;
XX DT 20-NOV-2003 (first entry)
XX DE Photorhabdus luminescens protein sequence #582.
XX KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX XX Photorhabdus luminescens.
OS WO200294867-A2.
XX PN 28-NOV-2002.
XX PD 07-FEB-2002; 2002WO-IB003040.
XX PF 07-FEB-2001; 2001FR-00001659.
XX PR (INSP) INST PASTEUR.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX WPI; 2003-148459/14.
XX XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX PS Claim 2; SEQ ID NO 582; 1205pp; French.
XX CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins
XX SQ Sequence 373 AA;
Query Match 100.0%; Score 86; DB 6; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 12
ADR89339
ID ADR89339 standard; protein; 376 AA.
XX AC ADR89339;
XX KW

DT 18-NOV-2004 (first entry)
XX DE E. coli protein-folding-related factor, DnaJ.
XX KW PFRF; protein-folding-related factor; chaperone; GroEL; DnaK;
KW DnaJ; GrpE; gene function; cell-free synthesis;
KW recombinant protein production; therapeutic protein.
XX OS Escherichia coli.
XX PN WO2004072107-A1.
XX PD 26-AUG-2004.
XX PF 13-FEB-2004; 2004WO-KR000302.
XX PR 15-FEB-2003; 2003KR-00009628.
XX PA (DREA-) DREAMBIOGEN CO LTD.
XX PI Kang SH, Choi WJ, Kim HJ, Jun SY, Lee KY;
XX WPI; 2004-616042/59.
XX PT Producing soluble proteins using transformed genes encoding protein-
PT folding-related factors in a cell-free protein synthesis system, useful
PT in therapeutic, industrial and research purposes.
XX PS Example 1; SEQ ID NO 4; 58pp; English.
XX CC The invention relates to producing soluble protein. The method involves
CC preparing cells transformed by genes encoding protein-folding-related
CC factors (PFRF), so that the transformed cells can express enhanced levels
CC of the PFRFs, over-expressing the factors and preparing a cell extract
CC for a cell-free protein synthesis system from the transformed cells, and
CC producing a high level of soluble protein in the synthesis system
CC containing the extract containing the factors. The folding-related factor
CC in producing a soluble protein is one or more in number, and/or is a
CC chaperone that is GroES/GroEL chaperone family or DnaK/DnaJ/GrpE
CC chaperone family. The cell extract is prepared from one or more
CC transformed cells. The protein is alpha, beta, gamma-interferon, lipase,
CC erythropoietin, cytokines, interleukins, granulocyte-colony stimulating
CC factor, granulocyte macrophage-colony stimulating factor, transforming
CC growth factors, thrombopoietin, or tissue plasminogen activator. The
CC methods and compositions of the present invention are useful for
CC producing soluble proteins applicable to therapeutic, industrial and
CC research purposes, in particular for assaying functions of newly
CC discovered genes. The present sequence represents the amino acid sequence
CC of an E. coli DnaJ, a protein-folding-related factor.
XX SQ Sequence 376 AA;
Query Match 100.0%; Score 86; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76
RESULT 13
ADN18036
ID ADN18036 standard; protein; 376 AA.
XX AC ADN18036;
XX DT 02-DEC-2004 (first entry)
XX DE Bacterial polypeptide #689.
XX KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 689; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 376 AA;

Query Match 100.0%; Score 86; DB 8; Length 376;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 14
ID ADN17733 standard; protein; 378 AA.
XX
AC ADN17733;

XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #386.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 386; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 86; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 15
ADS42875
ID ADS42875 standard; protein; 378 AA.
XX
AC ADS42875;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #21305.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 21305; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 86; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	86	100.0	16	14 US-10-001-938-3	Sequence 3, Appli
2	86	100.0	340	9 US-09-764-868-1153	Sequence 1153, Ap
3	86	100.0	341	9 US-09-764-868-1152	Sequence 1152, Ap
4	86	100.0	376	15 US-10-369-493-689	Sequence 689, App
5	86	100.0	378	15 US-10-369-493-386	Sequence 386, App
6	86	100.0	378	15 US-10-369-493-21305	Sequence 21305, A
7	81	94.2	15	9 US-09-756-983-10	Sequence 10, Appl
8	81	94.2	15	9 US-09-828-574-10	Sequence 10, Appl
9	81	94.2	15	14 US-10-001-938-27	Sequence 27, Appl
10	81	94.2	15	14 US-10-299-540-4	Sequence 4, Appli
11	81	94.2	15	14 US-10-299-184-4	Sequence 4, Appli
12	81	94.2	15	14 US-10-239-313A-444	Sequence 444, App
13	81	94.2	16	14 US-10-239-313A-447	Sequence 447, App

14	79	91.9	365	15	US-10-369-493-10648	Sequence 10648, A
15	78	90.7	376	15	US-10-369-493-12087	Sequence 12087, A
16	72	83.7	15	9	US-09-828-574-11	Sequence 11, Appl
17	72	83.7	15	14	US-10-299-540-5	Sequence 5, Appli
18	72	83.7	15	14	US-10-299-184-5	Sequence 5, Appli
19	69	80.2	382	15	US-10-369-493-8065	Sequence 8065, Ap
20	69	80.2	384	15	US-10-369-493-21849	Sequence 21849, A
21	67	77.9	376	16	US-10-375-010-22	Sequence 22, Appl
22	67	77.9	379	15	US-10-369-493-7330	Sequence 7330, Ap
23	67	77.9	380	15	US-10-369-493-4573	Sequence 4573, Ap
24	63	73.3	376	15	US-10-369-493-47	Sequence 47, Appl
25	62	72.1	374	15	US-10-369-493-13658	Sequence 13658, A
26	61	70.9	378	15	US-10-369-493-8450	Sequence 8450, Ap
27	60	69.8	368	9	US-09-861-451A-2	Sequence 2, Appli
28	60	69.8	375	15	US-10-369-493-15859	Sequence 15859, A
29	60	69.8	376	15	US-10-369-493-15487	Sequence 15487, A
30	59	68.6	358	15	US-10-369-493-9641	Sequence 9641, Ap
31	58	67.4	379	15	US-10-369-493-18523	Sequence 18523, A
32	58	67.4	385	15	US-10-369-493-16754	Sequence 16754, A
33	57	66.3	369	15	US-10-369-493-19646	Sequence 19646, A
34	56	65.1	362	15	US-10-369-493-9305	Sequence 9305, Ap
35	56	65.1	378	16	US-10-474-776-634	Sequence 634, App
36	56	65.1	378	17	US-10-472-928-900	Sequence 900, App
37	54	62.8	15	14	US-10-299-540-6	Sequence 6, Appli
38	54	62.8	15	14	US-10-299-184-6	Sequence 6, Appli
39	53	61.6	423	15	US-10-369-493-12619	Sequence 12619, A
40	52	60.5	360	15	US-10-369-493-10371	Sequence 10371, A
41	52	60.5	372	15	US-10-369-493-23206	Sequence 23206, A
42	52	60.5	376	15	US-10-369-493-1212	Sequence 1212, Ap
43	50	58.1	175	16	US-10-767-701-40315	Sequence 40315, A
44	50	58.1	297	15	US-10-282-122A-54551	Sequence 54551, A
45	50	58.1	362	16	US-10-437-963-190831	Sequence 190831,

ALIGNMENTS

RESULT 1

US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: ALBANI, Salvatore

; APPLICANT: CARSON, Dennis

; APPLICANT: PRAKKEN, Berent

; APPLICANT: MARTINI, Alberto

; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: UCSD1360-1

; CURRENT APPLICATION NUMBER: US/10/001,938

; CURRENT FILING DATE: 2001-10-31

; PRIOR APPLICATION NUMBER: US 60/245,181

; PRIOR FILING DATE: 2000-11-01

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.2e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QKRAAYDOYGHAAFEQ 16

RESULT 2

US-09-764-868-1153

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; Sequence 1153, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (196)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1153
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Query Match 100.0%; Score 86; DB 9; Length 340;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QKRAAYDQYGHAAFEQ 16
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Db 25 QKRAAYDQYGHAAFEQ 40
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RESULT 3
US-09-764-868-1152
; Sequence 1152, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1152
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-1152
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Query Match 100.0%; Score 86; DB 9; Length 341;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QKRAAYDQYGHAAFEQ 16
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Db 26 QKRAAYDQYGHAAFEQ 41
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RESULT 4
US-10-369-493-689
; Sequence 689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 689
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-369-493-689
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Query Match 100.0%; Score 86; DB 15; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QKRAAYDQYGHAAFEQ 16
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Db 61 QKRAAYDQYGHAAFEQ 76
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```
RESULT 5
US-10-369-493-386
; Sequence 386, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 386
; LENGTH: 378
; TYPE: PRT
; ORGANISM: xenorhabdus nematophilus
US-10-369-493-386
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Query Match 100.0%; Score 86; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76
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RESULT 6
US-10-369-493-21305
; Sequence 21305, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
```

; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21305
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-21305

Query Match 100.0%; Score 86; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | | | |
Db 61 QKRAAYDQYGHAAFEQ 76

RESULT 7
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
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Db 1 QKRAAYDQYGHAAFE 15

RESULT 8
US-09-828-574-10
; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKKEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1

; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaJPl peptide
US-09-828-574-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-10-001-938-27
; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-27

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 10
US-10-299-540-4
; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF R
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-540-4

Query Match
Best Local Similarity 94.2%; Score 81; DB 14; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
US-10-299-184-4
; Sequence 4, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-184-4

Query Match
Best Local Similarity 94.2%; Score 81; DB 14; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 12
US-10-239-313A-444
; Sequence 444, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie

; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-444

Query Match
Best Local Similarity 94.2%; Score 81; DB 14; Length 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 13
US-10-239-313A-447
; Sequence 447, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-447

Query Match
Best Local Similarity 94.2%; Score 81; DB 14; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 14
US-10-369-493-10648
; Sequence 10648, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 10648
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Spingomonas aromaticivorans
US-10-369-493-10648

Query Match 91.9%; Score 79; DB 15; Length 365;
Best Local Similarity 87.5%; Pred. No. 3.6e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
Db 56 QKRAAYDRYGHAAFEQ 71

RESULT 15
US-10-369-493-12087
; Sequence 12087, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12087
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12087

Query Match 90.7%; Score 78; DB 15; Length 376;
Best Local Similarity 87.5%; Pred. No. 5.5e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
Db 60 QKRAAYDRYGHAAFEQ 75

Search completed: March 7, 2005, 08:45:18
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:23:03 ; Search time 19.8146 Seconds
(without alignments)
60.278 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	86	100.0	131	3	US-09-553-498-4	Sequence 4, Appli
2	86	100.0	131	4	US-09-618-869-4	Sequence 4, Appli
3	86	100.0	380	4	US-09-543-681A-5912	Sequence 5912, Ap
4	86	100.0	380	4	US-09-489-039A-9011	Sequence 9011, Ap
5	86	100.0	399	3	US-09-553-498-2	Sequence 2, Appli
6	86	100.0	399	4	US-09-618-869-2	Sequence 2, Appli
7	81	94.2	15	1	US-08-618-464-4	Sequence 4, Appli
8	81	94.2	15	3	US-09-107-615-4	Sequence 4, Appli
9	81	94.2	15	4	US-09-756-983-10	Sequence 10, Appl
10	81	94.2	15	5	PCT-US95-04896-4	Sequence 4, Appli
11	72	83.7	15	1	US-08-618-464-5	Sequence 5, Appli
12	72	83.7	15	3	US-09-107-615-5	Sequence 5, Appli
13	72	83.7	15	5	PCT-US95-04896-5	Sequence 5, Appli
14	62	72.1	381	4	US-09-252-991A-27174	Sequence 27174, A
15	61	70.9	407	4	US-09-540-236-2899	Sequence 2899, Ap
16	60	69.8	368	4	US-09-861-451A-2	Sequence 2, Appli
17	56	65.1	352	2	US-08-472-534-6	Sequence 6, Appli
18	56	65.1	378	4	US-09-583-110-4647	Sequence 4647, Ap
19	56	65.1	379	4	US-09-107-433-3487	Sequence 3487, Ap
20	54	62.8	15	1	US-08-618-464-6	Sequence 6, Appli
21	54	62.8	15	3	US-09-107-615-6	Sequence 6, Appli
22	53	61.6	240	4	US-09-248-796A-17703	Sequence 17703, A
23	52	60.5	375	4	US-09-328-352-4984	Sequence 4984, Ap
24	47	54.7	138	4	US-09-902-540-13689	Sequence 13689, A
25	47	54.7	373	4	US-09-710-279-890	Sequence 890, App
26	47	54.7	385	3	US-09-134-001C-3688	Sequence 3688, Ap
27	46	53.5	419	2	US-08-686-417-3	Sequence 3, Appli

28	45	52.3	677	4	US-09-252-991A-18102	Sequence 18102, A
29	44	51.2	387	4	US-09-908-992B-11	Sequence 11, Appl
30	44	51.2	397	4	US-09-248-796A-17628	Sequence 17628, A
31	44	51.2	414	4	US-09-908-992B-10	Sequence 10, Appl
32	44	51.2	452	4	US-09-908-992B-29	Sequence 29, Appl
33	44	51.2	453	4	US-09-908-992B-9	Sequence 9, Appli
34	44	51.2	453	4	US-09-908-992B-30	Sequence 30, Appl
35	44	51.2	479	4	US-09-908-992B-28	Sequence 28, Appl
36	44	51.2	480	4	US-09-908-992B-8	Sequence 8, Appli
37	44	51.2	480	4	US-09-908-992B-12	Sequence 12, Appl
38	44	51.2	915	4	US-09-252-991A-24992	Sequence 24992, A
39	43	50.0	1895	2	US-08-619-554-4	Sequence 4, Appli
40	41	47.7	87	4	US-09-882-835-4	Sequence 4, Appli
41	41	47.7	223	4	US-09-658-644-4	Sequence 4, Appli
42	41	47.7	223	4	US-09-949-016-6832	Sequence 6832, Ap
43	41	47.7	267	4	US-09-949-016-11497	Sequence 11497, A
44	41	47.7	348	2	US-08-974-546-1	Sequence 1, Appli
45	41	47.7	387	4	US-09-543-681A-7130	Sequence 7130, Ap

ALIGNMENTS

RESULT 1
US-09-553-498-4
; Sequence 4, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-4

Query Match 100.0%; Score 86; DB 3; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
|||
Db 84 QKRAAYDQYGHAAFEQ 99

RESULT 2
US-09-618-869-4
; Sequence 4, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; TITLE OF INVENTION: CHAPERONES
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1


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; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-08-618-464-4

Query Match 94.2%; Score 81; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 8
US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-09-107-615-4

Query Match 94.2%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred.No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJpl heat shock protein
; US-09-756-983-10

Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred.No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15
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RESULT 10
PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; PCT-US95-04896-4

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
US-08-618-464-5
; Sequence 5, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; US-08-618-464-5

Query Match 83.7%; Score 72; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
: | | | | | | | | | | | | | | |
Db 2 ERAAYDQYGHAAFE 15

RESULT 12
US-09-107-615-5
; Sequence 5, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-09-107-615-5

Query Match 83.7%; Score 72; DB 3; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15

RESULT 13
PCT-US95-04896-5
Sequence 5, Application PC/TUS9504896
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: OF CALIFORNIA
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04896
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
FEATURE:
NAME/KEY: Peptide

LOCATION: 1..15
PCT-US95-04896-5
Query Match 83.7%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15
RESULT 14
US-09-252-991A-27174
Sequence 27174, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27174
LENGTH: 381
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27174

Query Match 72.1%; Score 62; DB 4; Length 381;
Best Local Similarity 78.6%; Pred. No. 0.0056;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
Db 66 KRAAYDQYGHAGVD 79

RESULT 15
US-09-540-236-2899
Sequence 2899, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2899
LENGTH: 407
TYPE: PRT
ORGANISM: M.catarrhalis
US-09-540-236-2899

Query Match 70.9%; Score 61; DB 4; Length 407;
Best Local Similarity 62.5%; Pred. No. 0.009;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
Db 84 EKRAYDRMGHSAYEQ 99

Search completed: March 7, 2005, 07:55:52
Job time : 20.8146 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run On: March 7, 2005, 09:43:27 ; Search time 38 Seconds
(without alignments)
40.512 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2773

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	39.5	11	2 A60656	perisulfakinin - A
2	34	39.5	14	2 A56632	neosulfakinin-II -
3	31	36.0	10	1 GMROL2	leucosulfakinin-II
4	31	36.0	10	2 B60656	leucosulfakinin II
5	31	36.0	13	2 S47372	T-cell antigen rec
6	31	36.0	13	2 S47384	T-cell antigen rec
7	30	34.9	11	1 GMROL	leucosulfakinin -
8	30	34.9	13	2 S47368	T-cell antigen rec
9	28	32.6	13	2 S47359	T-cell antigen rec
10	28	32.6	13	2 S47365	T-cell antigen rec
11	28	32.6	13	2 S47374	T-cell antigen rec
12	26	30.2	11	2 PT0214	T-cell receptor be
13	26	30.2	13	2 S47388	T-cell antigen rec
14	26	30.2	13	2 PH1479	T-cell receptor be
15	26	30.2	14	4 I52618	hemoglobin beta ch
16	26	30.2	15	2 PH0770	T-cell receptor be
17	25	29.1	13	2 S32471	lymnadFamide 1 - g
18	25	29.1	14	2 PH1586	Ig H chain V-D-J r
19	24	27.9	16	2 PH1622	Ig H chain V-D-J r
20	24	27.9	16	2 PH1589	Ig H chain V-D-J r
21	23	26.7	8	2 S11078	glucose-6-phosphat
22	23	26.7	13	2 S32472	lymnadFamide 2 - g
23	23	26.7	13	2 A60379	factor X activator
24	22	25.6	13	2 S47383	T-cell antigen rec
25	22	25.6	13	2 S32473	lymnadFamide 3 - g
26	22	25.6	15	2 PH1319	Ig heavy chain DJ
27	22	25.6	15	2 F28587	T-cell receptor be
28	22	25.6	15	2 I53284	T-cell receptor be
29	21	24.4	10	2 PT0215	T-cell receptor be

30	21	24.4	12	2 PH0746	T-cell receptor be
31	21	24.4	12	2 PH0771	T-cell receptor be
32	21	24.4	12	2 PH1461	T-cell receptor be
33	21	24.4	13	2 S47361	T-cell antigen rec
34	21	24.4	13	2 I51905	collecting duct wa
35	21	24.4	13	2 S32474	lymnadFamide 4 - g
36	21	24.4	14	2 S44957	photosystem II oxy
37	21	24.4	14	2 PH0755	T-cell receptor be
38	21	24.4	14	2 A17150	glucose 1-dehydrog
39	21	24.4	14	2 S48685	extension protein
40	21	24.4	15	2 PC4269	unidentified QR310
41	20	23.3	10	2 PT0309	Ig heavy chain CRD
42	20	23.3	13	2 G22565	R-phycoerythrin ga
43	20	23.3	13	2 PN0168	phosphopyruvate hy
44	20	23.3	14	2 PA0013	photosystem II oxy
45	20	23.3	14	2 PT0232	Ig heavy chain CRD

ALIGNMENTS

RESULT 1

A60656
perisulfakinin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A60656
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American
A;Reference number: A60656; MUID:90137190; PMID:2615921
A;Accession: A60656
A;Molecule type: protein
A;Residues: 1-11 <VEE>
A;Cross-references: UNIPROT:P36885
C;Comment: This neuropeptide stimulates hindgut contractions.
C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 8.8;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 3 FDDYGHMRF 11

RESULT 2

A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N;Alternate names: Neb-SK-II
N;Contains: neosulfakinin-I (Neb-SK-I)
C;Species: Sarcophaga bullata
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56632
R;Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992
A;Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf
A;Reference number: A56632; MUID:93083101; PMID:1360367
A;Accession: A56632
A;Molecule type: protein
A;Residues: 1-14 <FON>
A;Cross-references: UNIPROT:P41493
A;Experimental source: heads
A;Note: sequence extracted from NCBI backbone (NCBIP:120391)
C;Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F;1-14/Product: neosulfakinin-II #status experimental <NSK2>
F;6-14/Product: neosulfakinin-I #status experimental <NSK1>
F;9/Binding site: sulfate (Tyr) (covalent) #status predicted
F;14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
| | | | |
Db 6 FDDYGHMRF 14

RESULT 3
GMROL2
leucosulfakinin-II - Madeira cockroach
N;Alternate names: LSK-II
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26335
R;Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.
Biochem. Biophys. Res. Commun. 140, 357-364, 1986
A;Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to ch
A;Reference number: A26335; MUID:87048769; PMID:3778455
A;Accession: A26335
A;Molecule type: protein
A;Residues: 1-10 <NAC>
A;Cross-references: UNIPROT:P09039
C;Comment: This peptide was isolated from head extracts. It stimulates muscle contractio
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14
| | | | |
Db 3 DDYGHMRF 10

RESULT 4
B60656
leucosulfakinin II, non-sulfated - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: B60656
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American
A;Reference number: A60656; MUID:90137190; PMID:2615921
A;Accession: B60656
A;Molecule type: protein
A;Residues: 1-10 <VEE>
A;Cross-references: UNIPROT:P09039
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14
| | | | |
Db 3 DDYGHMRF 10

RESULT 5
S47372
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47372

R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A;Reference number: S47355
A;Accession: S47372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35697; NID:g527485; PIDN:CAA84766.1; PID:g527486
C;Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAAAYDQY 9
| | | | |
Db 6 RSAYEQY 12

RESULT 6
S47384
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47384
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A;Reference number: S47355
A;Accession: S47384
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35704; NID:g527501; PIDN:CAA84773.1; PID:g527502
C;Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAAAYDQY 9
| | | | |
Db 6 RSAYEQY 12

RESULT 7
GMROL
leucosulfakinin - Madeira cockroach
N;Alternate names: LSK
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch
A;Reference number: A01622; MUID:86315858; PMID:3749893
A;Accession: A01622
A;Molecule type: protein
A;Residues: 1-11 <NAC>
A;Cross-references: UNIPROT:P04428
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.9%; Score 30; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 44;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
| | | | |
Db 3 FEDYGHMRF 11

RESULT 8

S47368
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47368
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47368
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35693; NID:G527477; PIDN:CAA84762.1; PID:G527478
C:Keywords: T-cell receptor

Query Match 34.9%; Score 30; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RAAVDQY 9
|:::|
Db 6 RGAYEQY 12

RESULT 9

S47359
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47359
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47359
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PID:G527456
C:Keywords: T-cell receptor

Query Match 32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RAAVDQY 9
|:::|
Db 6 RSSYEQY 12

RESULT 10

S47365
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47365
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PID:G527472; EMBL:Z35679;
A:Accession: S47375
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>

A:Cross-references: EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PID:G527494
A:Accession: S47379
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE3>
A:Cross-references: EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PID:G527510
A:Accession: S47396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PID:G527528
A:Accession: S47397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PID:G527530
A:Accession: S47398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PID:G527532
C:Keywords: T-cell receptor

Query Match 32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RAAVDQY 9
|:::|
Db 6 RSSYEQY 12

RESULT 11

S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: S47374; S47399; S47364
R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>

A:Cross-references: EMBL:Z35699; NID:G527491; PIDN:CAA84768.1; PID:G527492; EMBL:Z35689;
A:Accession: S47399
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: EMBL:Z35677; NID:G527533; PIDN:CAA84746.1; PID:G527534
C:Keywords: T-cell receptor

Query Match 32.6%; Score 28; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RAAVDQY 9
|:::|
Db 6 RSSYEQY 12

RESULT 12

PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0214
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214
A;Molecule type: mRNA
A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor

Query Match 30.2%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAAVDQY 9
| | | | |
Db 4 RGTVEQY 10

RESULT 13
S47388
T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47388
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number: S47355
A;Accession: S47388
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35710; NID:G527510; PIDN:CAA84779.1; PID:G527516
C;Keywords: T-cell receptor

Query Match 30.2%; Score 26; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RAAVDQY 9
| | | | |
Db 6 RAAVEQY 12

RESULT 14
PH1479
T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C;Accession: PH1479
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1479
A;Molecule type: mRNA
A;Residues: 1-13 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Keywords: receptor; T-cell

Query Match 30.2%; Score 26; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RAAVDQY 9
| | | | |
Db 5 QAGVEQY 11

RESULT 15
I52618
hemoglobin beta chain thalassemia mutant Portuguese - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000
C;Accession: I52618
R;Oner, R.; Oner, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huisman, T.H.
Br. J. Haematol. 79, 306-310, 1991

A;Title: Dominant beta-thalassaemia trait in a Portuguese family is caused by a deletion
A;Reference number: I52618; MUID:92068764; PMID:1659862
A;Accession: I52618
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14 <ONE>
A;Cross-references: GB:S68042; NID:G239717; PIDN:AAB20440.1; PID:G239718
C;Genetics:
A;Gene: GDB:HBB
A;Cross-references: GDB:119297; OMIM:141900
A;Map position: 11p15.4-11p15.4

Query Match 30.2%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RAAVDQYGH 12
: | | | : | | |
Db 4 QAAVQKVGRA 13

Search completed: March 7, 2005, 09:58:38
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 09:10:02 ; Search time 172 Seconds
(without alignments)
47.635 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 7514

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	39.5	9	1	NSK1_SARBU
2	34	39.5	11	1	LSKP_PERAM
3	34	39.5	14	1	NSK2_SARBU
4	33	38.4	12	1	LOSK_LOCMI
5	31	36.0	10	1	LSK2_LEUMA
6	31	36.0	10	1	LSK2_PERAM
7	30	34.9	11	1	LSK1_LEUMA
8	25	29.1	13	1	NP1_LYMST
9	24	27.9	13	2	Q7S2J9
10	24	27.9	16	2	O82402
11	24	27.9	16	2	O82404
12	24	27.9	16	2	O82405
13	24	27.9	16	2	O82406
14	24	27.9	16	2	O82407
15	24	27.9	16	2	O82781
16	23	26.7	13	1	NP2_LYMST
17	23	26.7	13	2	Q7LZ24
18	22.5	26.2	16	2	Q9S8A0
19	22	25.6	10	2	Q71UL3
20	22	25.6	11	2	Q68D59
21	22	25.6	13	1	NP3_LYMST
22	22	25.6	13	2	Q6URV3
23	22	25.6	15	2	Q9TNP2
24	22	25.6	16	2	Q9S898
25	21	24.4	13	1	NP4_LYMST
26	21	24.4	13	1	PSBP_PINPS
27	21	24.4	13	2	Q80Y03
28	21	24.4	14	2	Q7M0K1
29	21	24.4	15	1	ECDA_LYMDI
30	21	24.4	16	2	Q9TRR1
31	20	23.3	9	2	Q93LE4

32	20	23.3	11	2	O60614	O60614 homo sapien
33	20	23.3	11	2	Q9TWM2	Q9twm2 aplysia cal
34	20	23.3	11	2	P89269	P89269 xestia c-ni
35	20	23.3	12	2	O46664	O46664 macropus ro
36	20	23.3	12	2	Q9QVF2	Q9qvf2 rattus sp.
37	20	23.3	13	2	Q7M4Y6	Q7m4y6 fusarium sp
38	20	23.3	13	2	Q7M268	Q7m268 gastrocioni
39	20	23.3	14	2	Q9FYT0	Q9fyto allium cepa
40	20	23.3	15	2	Q7M4Z3	Q7m4z3 fusarium sp
41	20	23.3	15	2	Q9S8I1	Q9s8i1 volvox cart
42	20	23.3	15	2	Q9JP39	Q9jp39 pseudomonas
43	20	23.3	15	2	Q7M0G8	Q7m0g8 mus sp. cd3
44	20	23.3	16	2	Q6XA08	Q6xa08 equus cabal
45	20	23.3	16	2	O82403	O82403 fragaria ve

ALIGNMENTS

RESULT 1

NSK1_SARBU	STANDARD;	PRT;	9 AA.
ID NSK1_SARBU			
AC P41492;			
DT 01-NOV-1995 (Rel. 32, Created)			
DT 01-NOV-1995 (Rel. 32, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DE Neosulfakinin-I (NEB-SK-I).			
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;			
OC Sarcophagidae; Sarcophaga.			
OX NCBI_TaxID=7385;			
RN [1]			
RP SEQUENCE.			
RC TISSUE=Head;			
RX MEDLINE=93083101; PubMed=1360367;			
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;			
RT "Isolation and primary structure of two sulfakinin-like peptides from			
RL the fleshfly, Neobellieria bullata.";			
RL Comp. Biochem. Physiol. 103C:135-142(1992).			
CC -1- FUNCTION: Myotropic peptide.			
CC -1- SUBCELLULAR LOCATION: Secreted.			
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.			
DR InterPro; IPR001651; Gastrin.			
DR PROSITE; PS00259; GASTRIN; 1.			
KW Amidation; Direct protein sequencing; Neuropeptide; Sulfation.			
FT MOD_RES 4 4 Sulfotyrosine (Potential).			
FT MOD_RES 9 9 Phenylalanine amide (Potential).			
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;			

Query Match 39.5%; Score 34; DB 1; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14

Db 1 FDDYGHMRF 9

RESULT 2

LSKP_PERAM	STANDARD;	PRT;	11 AA.
ID LSKP_PERAM			
AC P36885;			
DT 01-JUN-1994 (Rel. 29, Created)			
DT 01-JUN-1994 (Rel. 29, Last sequence update)			
DT 05-JUL-2004 (Rel. 44, Last annotation update)			
DE Perisulfakinin (Pea-SK-I).			
OS Periplaneta americana (American cockroach).			
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;			
OC Blattidae; Periplaneta.			
OX NCBI_TaxID=6978;			
RN [1]			

RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: Stimulates hindgut contractions.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6 6 Sulfotyrosine.
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 39.5%; Score 34; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 3 FDDYGHMRF 11

RESULT 3
NSK2_SARBU
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -!- FUNCTION: Myotropic peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Neuropeptide; Sulfation.
FT MOD_RES 9 9 Sulfotyrosine (Potential).
FT MOD_RES 14 14 Phenylalanine amide (Potential).
SQ SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match 39.5%; Score 34; DB 1; Length 14;
Best Local Similarity 55.6%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 6 FDDYGHMRF 14

RESULT 4
LOSK_LOCMI
ID LOSK_LOCMI STANDARD; PRT; 12 AA.
AC P47733;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sulfakinin (LOM-SK).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
RL (In) McCaffery A., Wilson I. (eds.);
RL Chromatography and isolation of insect hormones and pheromones,
RL pp.231-241, Plenum Press, New York (1990).
CC -!- FUNCTION: Myotropic peptide.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 7 7 Sulfotyrosine (Potential).
FT MOD_RES 12 12 Phenylalanine amide.
SQ SEQUENCE 12 AA; 1440 MW; 9B5B5DA9BD6B5AAA CRC64;

Query Match 38.4%; Score 33; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 AYDQYGHAAF 14
Db 3 ASDDYGHMRF 12

RESULT 5
LSK2_LEUMA
ID LSK2_LEUMA STANDARD; PRT; 10 AA.
AC P67802; P09039;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucosulfakinin-II (LSK-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=87048769; PubMed=3778455;
RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
RT homology to cholecystokinin and gastrin.";
RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
CC -!- FUNCTION: Changes the frequency and amplitude of contractions of
CC the cockroach hingut. Stimulates muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A26335; GMROL2.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 5 5 Sulfotyrosine.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;

Query Match 36.0%; Score 31; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAAF 14

```
Db          3 DDYGHMRF 10

RESULT 6
LSK2_PERAM
ID LSK2_PERAM STANDARD; PRT; 10 AA.
AC P67803; P09039;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leucosulfakinin-II (LSK-II).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
RA Veestra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: Changes the frequency and amplitude of contractions of
CC the cockroach hindgut. Stimulates muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; B60656; B60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;

Query Match 36.0%; Score 31; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          7 DQYGHAAF 14
| | | | |
Db          3 DDYGHMRF 10

RESULT 7
LSK1_LEUMA
ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: Changes the frequency and amplitude of contractions of
CC the hindgut. Inhibits muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6 6 Sulfotyrosine.
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```
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 34.9%; Score 30; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY          6 YDQYGHAAF 14
| | | | |
Db          3 FEDYGHMRF 11

RESULT 8
NP1_LYMST
ID NP1_LYMST STANDARD; PRT; 13 AA.
AC P80178;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lymnaea-DF-amide 1.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
SEQUENCE.
RC TISSUE=Ganglion; PubMed=8477756;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "Lymnaeidae, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Related to the cholecystokinin (CKK) family.
DR PIR; S32471; S32471.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 13 13 Phenylalanine amide.
SQ SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;

Query Match 29.1%; Score 25; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY          6 YDQYGHAAF 14
| | | | |
Db          2 YDRISNSAF 10

RESULT 9
Q7S2J9
ID Q7S2J9 PRELIMINARY; PRT; 13 AA.
AC Q7S2J9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU04977.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Taffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Biele C., Rudd S., Frishman D.,
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RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbola D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000422; EAA29651.1; -.
SQ SEQUENCE 13 AA; 1703 MW; 099245360492586B CRC64;

Query Match 27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 AYDQYGHAAF 14
Db 2 AIDYYGYCY 11

RESULT 10
O82402 PRELIMINARY; PRT; 16 AA.
AC O82402;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria nubicola.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=60188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA520;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000213; AAC36540.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
Db 10 YGHEA 14

RESULT 11
O82404 PRELIMINARY; PRT; 16 AA.
AC O82404;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria nilgerrensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64941;
```

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berlin 1;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000217; AAC36544.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
Db 10 YGHEA 14

RESULT 12
O82405 PRELIMINARY; PRT; 16 AA.
AC O82405;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria innumae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64939;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRA 377;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000218; AAC36545.1; -.
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
Db 10 YGHEA 14

RESULT 13
O82406 PRELIMINARY; PRT; 16 AA.
AC O82406;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria moschata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64940;
RN [1]
```


RP SEQUENCE FROM N.A.
RC STRAIN=FRA 157;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF000219; AAC36546.1; --
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
|||
Db 10 YGHEA 14

RESULT 14

O82407 PRELIMINARY; PRT; 16 AA.
AC O82407;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria viridis (Wild strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=64942;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=FRA 341;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF000220; AAC36547.1; --
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
|||
Db 10 YGHEA 14

RESULT 15

O82781 PRELIMINARY; PRT; 16 AA.
AC O82781;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
GN Name=ADH;
OS Fragaria vesca (Woodland strawberry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
OX NCBI_TaxID=57918;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Yellow Wonder, and Baron Solemacher;
RA Yu H., Davis T.M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF000216; AAC36543.1; --
DR EMBL; AF000214; AAC36541.1; --
DR GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;

Query Match 27.9%; Score 24; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 YGHAA 13
|||
Db 10 YGHEA 14

Search completed: March 7, 2005, 09:57:54
Job time : 173 secs

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OM protein - protein search, using sw model

Run on: March 7, 2005, 09:07:16 ; Search time 159 Seconds
(without alignments)
38.919 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAFFQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 649094

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5	AAU98852 E.Coli DN
2	86	100.0	16	6	ABR55126 E. coli d
3	81	94.2	15	2	AAW25795 Peptide d
4	81	94.2	15	3	AAY79543 E. coli d
5	81	94.2	15	4	AAM99341 Vaccine r
6	81	94.2	15	5	AAU09842 E.coli dn
7	81	94.2	15	5	AAU98876 E. coli D
8	81	94.2	15	5	AAE19457 Human hea
9	81	94.2	15	6	ABR55132 E. coli D
10	81	94.2	16	4	AAM99344 Vaccine r
11	72	83.7	15	2	AAR95446 RA suscep
12	72	83.7	15	2	AAW25796 Peptide d
13	72	83.7	15	5	AAE19458 Heat shoc
14	72	83.7	15	6	ABR55133 E. coli d
15	64.5	75.0	14	2	AAR95445 RA suscep
16	54	62.8	15	2	AAW25798 Peptide d
17	54	62.8	15	6	ABR55123 E. coli d
18	34	39.5	9	4	AAU03347 Fruit fly
19	34	39.5	9	4	AAU03346 Fruit fly
20	34	39.5	9	4	AAU03351 Fruit fly
21	34	39.5	9	7	ADE14680 Drosulfak
22	34	39.5	9	7	ADE14676 DmGPCR bi
23	34	39.5	9	7	ADE14679 DmGPCR bi
24	34	39.5	9	7	ADE14677 DmGPCR bi
25	34	39.5	9	7	ADL83524 Drosophil

26	34	39.5	9	7	ADL83525	Adl83525 Drosophil
27	34	39.5	9	7	ADL83602	Adl83602 Drosophil
28	34	39.5	9	7	ADL83603	Adl83603 Drosophil
29	34	39.5	9	7	ADL83528	Adl83528 Drosophil
30	34	39.5	9	7	ADL83527	Adl83527 Drosophil
31	34	39.5	9	8	ADR03247	Adr03247 G-protein
32	34	39.5	9	8	ADR03249	Adr03249 G-protein
33	34	39.5	9	8	ADR03245	Adr03245 G-protein
34	34	39.5	9	8	ADR03248	Adr03248 G-protein
35	34	39.5	9	8	ADR03244	Adr03244 G-protein
36	34	39.5	14	3	AAB14081	Aab14081 Human HLA
37	34	39.5	14	4	AAU03353	Aau03353 Fruit fly
38	34	39.5	14	6	AAG79793	Aag79793 Peptide 6
39	34	39.5	14	7	ADE14681	Adel4681 Drosulfak
40	34	39.5	14	7	ADL83529	Adl83529 Drosophil
41	34	39.5	14	8	ADR03251	Adr03251 Drosophil
42	34	39.5	14	8	ADR03250	Adr03250 Drosophil
43	34	39.5	15	2	AAR10086	Aar10086 HLA Dw4 i
44	34	39.5	15	2	AAR10089	Aar10089 HLA Dw4p
45	34	39.5	15	2	AAW25799	Aaw25799 Synthetic

ALIGNMENTS

RESULT 1
AAU98852
ID AAU98852 standard; peptide; 16 AA.
XX
AC AAU98852;
XX
DT 22-AUG-2002 (first entry)
XX
DE E.Coli DNAJ 61 immunogenic peptide.
XX
KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytostatic; antiinflammatory; antibacterial; antiarthritic;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer;
KW mucosal tolerisation; DNA vaccination; anergy induction.
XX
OS Escherichia coli.
XX
PN WO200236611-A2.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-US045344.
XX
PR 01-NOV-2000; 2000US-0245181P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (MART/) MARTINI A.
XX
PI Martini A, Albani S, Carson DA, Prakken BJ;
XX
DR WPI; 2002-489999/52.
XX
PT New immunomodulatory peptides from heat shock proteins, useful for
PT treating immunological disorder in subjects such as humans, e.g.
PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
PT bowel disease or cancer.
XX
PS Claim 4; Page 55; 84pp; English.
XX
CC This invention relates to the use of a peptide, which is an immunogenic
CC portion derived from a dnaJ heat shock protein (hsp) in modulating an
CC immune response in a subject. The peptides of the invention may have
CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
CC antiarthritic properties and can stimulate expression of interleukins,
CC tumour necrosis factor and transforming growth factor beta. The
CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
CC reducing/inhibiting) an immune response in a subject having an

CC immunological disorder (e.g. autoimmune disease such as arthritis or
CC articular juvenile idiopathic arthritis), an infectious disease, an
CC inflammatory bowel disease or cancer. The immunogenic peptide of the
CC invention is also useful for modulating immunoeffector cell
CC responsiveness in a subject. The immunogenic peptide is particularly
CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
CC general, the peptide is useful in methods involving mucosal tolerisation,
CC DNA vaccination, anergy induction or active immunisation. The present
CC sequence represents an E. coli DNAJ immunogenic peptide of the invention
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
ABR55126
ID ABR55126 standard; peptide; 16 AA.
XX
AC ABR55126;
XX
DT 03-JUL-2003 (first entry)
XX
DE E. coli dnaJ61 antigen-specific epitope peptide.
XX
KW Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytostatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW antiallergic; dermatological; antipsoriatic.

XX
OS Escherichia coli.
XX
PN WO2003026579-A2.
XX
PD 03-APR-2003.

XX
PF 25-SEP-2002; 2002WO-US030578.
XX
PR 25-SEP-2001; 2001US-0325499P.
PR 11-DEC-2001; 2001US-0339284P.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Albani S, Martins A;
XX
DR WPI; 2003-430097/40.

XX
PT Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.

XX
PS Disclosure; Page 9; 41pp; English.

XX
CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the

CC invention
XX Sequence 16 AA;
SQ
Query Match 100.0%; Score 86; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFEQ 16
| | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 3
AAW25795
ID AAW25795 standard; peptide; 15 AA.
XX
AC AAW25795;

XX
DT 06-APR-1998 (first entry)
XX
DE Peptide dnaJp1 which protects against arthritogenic peptides.

XX
KW dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
KW arthritogenic peptide; autoimmune disease; systemic immune system;
KW anti-dnaJp1 antibody; passive immunisation;
KW rheumatoid arthritis-susceptibility detection.

XX
OS Escherichia coli.

XX
PN WO9734002-A1.

XX
PD 18-SEP-1997.

XX
PF 20-FEB-1997; 97WO-US002957.

XX
PR 15-MAR-1996; 96US-00618464.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Carson DA, Albani S;

XX
DR WPI; 1997-470882/43.

XX
PT Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
PT - also determining pre-disposition to rheumatoid arthritis by detecting
PT anti-arthritogenic peptide antibodies.

XX
PS Disclosure; Page 5; 44pp; English.

XX
CC Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
CC relatively strong immune response in seropositive adult rheumatoid
CC arthritis patients. This peptide was used in a vaccine for protecting
CC against arthritogenic peptides. The vaccine contains a carrier, pure
CC dnaJp1 peptide or a recombinant gene expression vector encoding the
CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
CC other autoimmune diseases). Vaccines can target the arthritogenic
CC peptides before they are presented to the systemic immune system. Anti-
CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies
CC can be used to detect rheumatoid arthritis-susceptibility sequences on
CC HLA or in populations of E. coli in the gastrointestinal tract

XX
SQ Sequence 15 AA;

Query Match 94.2%; Score 81; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

```
RESULT 4
AA79543
ID AAY79543 standard; peptide; 15 AA.
XX AC
XX AAY79543;
XX 15-AUG-2000 (first entry)
DE E. coli dnaJp1 heat shock protein peptide.
XX KW
XX KW Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator;
KW autoimmune disease; allergy; cancer; infection; graft rejection;
KW immunotherapy; therapy; major histocompatibility complex; MHC; dnaJp1;
KW heat shock protein.
XX XX
OS Escherichia coli.
XX PN
XX WO200023053-A2.
XX PD
XX 27-APR-2000.
XX PF
XX 19-OCT-1999; 99WO-US024666.
XX PR
XX 20-OCT-1998; 98US-0105018P.
XX PA (ALBA/) ALBANI S.
XX XX
XX PI Albani S;
XX DR
XX WPI; 2000-339492/29.
XX PT New artificial antigen presenting cells useful for isolating and
PT expanding T cells, and modulating T cell responses for the treatment of
PT e.g. autoimmune diseases, allergies.
XX XX
PS Disclosure; Page 42; 179pp; English.
XX CC
XX This peptide is derived from Escherichia coli heat shock protein dnaJp1.
CC Novel artificial antigen presenting cells (APC) of the invention comprise
CC antigens, such as the present peptide, that are presented by a major
CC histocompatibility complex (MHC) component for contact with, and
CC recognition by, a T cell receptor. The invention is directed to
CC artificial APC and methods of making APC, which are used to isolate and
CC expand T cell populations and to modulate T cell responses. The invention
CC also provides novel methods for the identification and isolation and
CC antigen-specific T cells. The methods provide for the construction of
CC liposomes containing MHC:peptide complexes, accessory molecules, co-
CC stimulatory molecules, adhesion molecules, and other molecules irrelevant
CC to T cell binding or modulation that are used in the binding of
CC artificial APC to solid support systems that may be used in the retrieval
CC and identification and antigen-specific T cells. Devices and methods are
CC provided for treating conditions that would benefit from modulation of T
CC cell response, e.g. autoimmune disorders (especially type I diabetes
CC mellitus, multiple sclerosis, rheumatoid arthritis, dermatomyositis,
CC juvenile rheumatoid arthritis and uveitis), allergies, cancer, viral
CC infections, and graft rejection
XX XX
SQ Sequence 15 AA;
Query Match 94.2%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15
RESULT 5
AAM99341
ID AAM99341 standard; peptide; 15 AA.
XX XX
```

```
AC AAM99341;
XX 07-DEC-2001 (first entry)
XX Vaccine related MHC ligand peptide SEQ ID NO:444.
DE XX
XX Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
KW human immunodeficiency virus.
XX XX
OS Homo sapiens.
XX PN
XX WO200170772-A2.
XX PD
XX 27-SEP-2001.
XX PF
XX 22-MAR-2001; 2001WO-FR000872.
XX PR
XX 23-MAR-2000; 2000FR-00003711.
XX PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX XX
XX PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX DR WPI; 2001-611470/70.
XX PT Stabilized pharmaceutical containing N-terminal glutamic acid or
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
PT with strong acid.
XX XX
PS Claim 9; Page 107; 149pp; French.
XX CC
XX The present invention describes a pharmaceutical compound (I) that
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
CC the form of an addition salt with a strong, physiologically acceptable
CC acid (II). Also described are: (a) a pharmaceutical composition
CC containing at least one (I); (b) a vaccine containing at least one (I)
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
CC method for in vitro diagnosis of diseases associated with the presence of
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
CC cytostatic activities. (I) are useful, in human or veterinary medicine,
CC in pharmaceutical compositions (for treating immune disorders, e.g.
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
CC rejection, infection, hormonal disorders and central nervous system
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
CC infections; or (ii) of cancers. A particular application is in anti-
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
CC associated with interactions between MHC and (I), e.g. melanoma and human
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
CC which can be used in pharmaceutical compounds from the present invention
XX XX
SQ Sequence 15 AA;
Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15
RESULT 6
AAU09842
ID AAU09842 standard; peptide; 15 AA.
XX XX
```


AC AAU09842;
XX
DT 26-FEB-2002 (first entry)
XX
DE E.coli dnaJp1 heat shock protein-derived peptide.
XX
KW Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; ophthalmological; antiallergic;
KW cytostatic; virucide; antibacterial; artificial antigen presenting cell;
KW liposome; major histocompatibility complex; MHC; T cell; allograft;
KW cytokine production; T-helper 2 response; transplantation therapy;
KW autoimmune disease; type I diabetes mellitus; multiple sclerosis;
KW rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis;
KW uveitis; allergy; cancer; infection; dnaJp1 heat shock protein.
XX
OS Escherichia coli.
XX
PN WO200180833-A1.
XX
PN 01-NOV-2001.
PD
XX
PF 20-APR-2000; 2000WO-IT000161.
XX
XX
PR 20-APR-2000; 2000WO-IT000161.
XX
PA (ALBA/) ALBANI S.
XX
PI Albani S;
XX
DR WPI; 2002-055316/07.
XX
PT New artificial antigen presenting cell, useful for modulating T cell
PT response for treating allergies and cancers, comprises liposome, major
PT histocompatibility complex, antigen and accessory molecule components.
XX
PS Disclosure; Page 46; 195pp; English.
XX
CC The invention relates to an artificial antigen presenting cell (I)
CC comprising liposome, major histocompatibility complex (MHC), antigen and
CC accessory molecule components. (I) is used in methods for the following:
CC (1) identifying T cells specific for an antigen of interest; (2)
CC isolating T cells specific for an antigen of interest; (3) modulating T
CC cell response; (4) characterising the functional state of antigen-
CC specific T cells; (5) treating a condition in a subject which would be
CC benefited by altering the functional pattern of cytokine production by
CC certain antigen-specific T cells to increase T-helper (Th) 2 response
CC and/or decrease Th1 response; (6) identifying antigen-specific T cells
CC specific for epitopes on a graft donor's tissue likely to elicit graft
CC versus host rejection response; and (7) treating a recipient mammal to
CC reduce rejection of allografts in a transplantation therapy regime.
CC Method (5) is useful for treating autoimmune disease such as type I
CC diabetes mellitus, multiple sclerosis, rheumatoid arthritis,
CC dermatomyositis, juvenile rheumatoid arthritis or uveitis. Alternatively
CC it is useful for treating allergy due to allergens such as dust, animal
CC skin bypass products, vegetables, fruits, pollen or chemicals, cancer,
CC viral infection, bacterial infection. Addition of the accessory
CC molecules, as well as co-stimulatory molecules, and other proteins in
CC proper orientation in the liposomes allow for substantially improved
CC binding association and manipulation of T cells which is very important
CC in the identification and stimulation of antigen-specific T cells. The
CC present sequence represents E.coli dnaJp1 heat shock protein-derived
XX peptide used in the method of the invention
SQ Sequence 15 AA;

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 7
AAU98876
ID AAU98876 standard; peptide; 15 AA.
XX
AC AAU98876;
XX
DT 22-AUG-2002 (first entry)
XX
DE E. coli DNAJ PI immunogenic peptide.
XX
KW Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
KW cytostatic; antiinflammatory; antibacterial; antiarthritic; human;
KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
KW infectious disease; inflammatory bowel disease; cancer; HDJ2;
KW mucosal tolerisation; DNA vaccination; anergy induction.
XX
OS Escherichia coli.
XX
PN WO200236611-A2.
XX
PN 10-MAY-2002.
PD
XX
PF 31-OCT-2001; 2001WO-US045344.
XX
PR 01-NOV-2000; 2000US-0245181P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (MART/) MARTINI A.
XX
PI Martini A, Albani S, Carson DA, Prakken BJ;
XX WPI; 2002-489999/52.
DR
XX
PT New immunomodulatory peptides from heat shock proteins, useful for
PT treating immunological disorder in subjects such as humans, e.g.
PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
PT bowel disease or cancer.
XX
XX Example 8; Page 53; 84pp; English.
CC This invention relates to the use of a peptide, which is an immunogenic
CC portion derived from a dnaJ heat shock protein (hsp) in modulating an
CC immune response in a subject. The peptides of the invention may have
CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
CC antiarthritic properties and can stimulate expression of interleukins,
CC tumour necrosis factor and transforming growth factor beta. The
CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing or
CC reducing/inhibiting) an immune response in a subject having an
CC immunological disorder (e.g. autoimmune disease such as arthritis or
CC articular juvenile idiopathic arthritis), an infectious disease, an
CC inflammatory bowel disease or cancer. The immunogenic peptide of the
CC invention is also useful for modulating immunoeffector cell
CC responsiveness in a subject. The immunogenic peptide is particularly
CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
CC general, the peptide is useful in methods involving mucosal tolerisation,
CC DNA vaccination, anergy induction or active immunisation. The present
CC sequence represents the E.coli DNAJ PI immunogenic peptide of the
XX invention
SQ Sequence 15 AA;

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

AAE19457
ID AAE19457 standard; peptide; 15 AA.
XX
AC AAE19457;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human heat shock protein (hsp) dnaJp1 peptide.
XX
KW Human; human leukocyte antigen; HLA; DR-binding peptide; therapy;
KW stress protein; major histocompatibility complex; MHC; antiulcer;
KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
KW ulcerative colitis; infectious disease; haemostatic; nephrotropic;
KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
KW inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
KW antiinfertility; idiopathic Addison's disease; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200212286-A2.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-US041656.
XX
PR 09-AUG-2000; 2000US-0224104P.
PR 06-APR-2001; 2001US-00828574.
XX
PA (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX
PI Albani S, Prakken BJ;
XX
DR WPI; 2002-227137/28.
XX
PT Novel human leukocyte antigen pan DR-binding peptide, useful for treating
PT immune mediated diseases and conditions, has a fragment of stress protein
PT that binds to major histocompatibility complex class II molecules.
XX
PS Claim 9; Page 45; 68pp; English.
XX
CC The invention relates to human leukocyte antigen (HLA) pan DR-binding
CC peptide comprising a fragment of a stress protein that binds to one or
CC more major histocompatibility complex (MHC) class II molecules. The
CC invention also relates to heat shock protein (hsp) peptides. The peptides
CC of the invention and the immunomodulating composition comprising these
CC peptides are useful for modulating, treating or preventing an immune-
CC mediated disease in a mammalian subject e.g. human, having or at risk of
CC having a disease including autoimmune disease, multiple sclerosis (MS),
CC rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
CC diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
CC lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
CC retinoblastoma, sarcoma and connective tissue cancers) and infectious
CC diseases. The peptides of the invention are also useful for screening
CC peptides or analogues that modulate pathogenic immune response. These
CC peptides are useful for treating autoimmune diseases or disorders
CC including Sjogren's syndrome, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, primary biliary cirrhosis, pernicious
CC anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease,
CC gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
CC disease, autoimmune neutropaenia, idiopathic thrombocytopenia purpura,
CC pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
CC bullous pemphigoid, discoid lupus and dense deposit disease. The present
CC sequence is human hsp dnaJp1 peptide used in the exemplification of the
XX invention
XX
SQ Sequence 15 AA;

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
ABR55132
ID ABR55132 standard; peptide; 15 AA.
XX
AC ABR55132;
XX
DT 03-JUL-2003 (first entry)
XX
DE E. coli DnaJp1 antigen-specific epitope peptide.
XX
KW Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytostatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW anti-allergic; dermatological; antipsoriatic.
XX
OS Escherichia coli.
XX
PN WO2003026579-A2.
XX
PD 03-APR-2003.
XX
PF 25-SEP-2002; 2002WO-US030578.
XX
PR 25-SEP-2001; 2001US-0325499P.
PR 11-DEC-2001; 2001US-0339284P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Albani S, Martins A;
XX
DR WPI; 2003-430097/40.
XX
PT Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.
XX
PS Disclosure; Page 9; 41pp; English.
XX
CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytostatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
XX invention
XX
SQ Sequence 15 AA;

Query Match 94.2%; Score 81; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 10
AAM99344

ID AAM99344 standard; peptide; 16 AA.
XX
AC AAM99344;
XX
DT 07-DEC-2001 (first entry)
XX
DE Vaccine related MHC ligand peptide SEQ ID NO:447.
XX
KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
KW human immunodeficiency virus.
XX
OS Homo sapiens.
XX
PN WO200170772-A2.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-FR000872.
XX
PR 23-MAR-2000; 2000FR-00003711.
XX
PA (FABR) FABRE MEDICAMENT SA PIERRE.
XX
PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
XX WPI; 2001-611470/70.
XX
PT Stabilized pharmaceutical containing N-terminal glutamic acid or
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
PT with strong acid.
XX
PS Claim 9; Page 107; 149pp; French.
XX
CC The present invention describes a pharmaceutical compound (I) that
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
CC the form of an addition salt with a strong, physiologically acceptable
CC acid (II). Also described are: (a) a vaccine containing at least one (I)
CC containing at least one (I); (b) a vaccine containing at least one (I)
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
CC method for in vitro diagnosis of diseases associated with the presence of
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
CC cytostatic activities. (I) are useful, in human or veterinary medicine,
CC in pharmaceutical compositions (for treating immune disorders, e.g.
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
CC rejection, infection, hormonal disorders and central nervous system
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
CC infections; or (ii) of cancers. A particular application is in anti-
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
CC associated with interactions between MHC and (I), e.g. melanoma and human
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
CC which can be used in pharmaceutical compounds from the present invention
XX
SQ Sequence 16 AA;

Query Match 94.2%; Score 81; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 11
AAR95446

ID AAR95446 standard; peptide; 15 AA.
XX
AC AAR95446;
XX
DT 01-JUL-1996 (first entry)
XX
DE RA susceptibility sequence peptide #2.
XX
KW Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;
KW arthritogenic peptide; RA-beggn bacteria; Escherichia; Lactococcus;
KW Klebsiella; Proteus; therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
XX Region 1. .5
FT /note= "rheumatoid arthritis susceptibility sequence"
FT Misc-difference 1 /note= "Q1D"
FT Misc-difference 2 /note= "K2E"
XX
PN WO9531984-A1.
XX
PD 30-NOV-1995.
XX
PF 24-APR-1995; 95WO-US004896.
XX
PR 20-MAY-1994; 94US-00246988.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Salvatore A;
XX WPI; 1996-020344/02.
XX
PT Treatment of rheumatoid arthritis - by limiting exposure of immune system
PT to arthritogenic peptide(s).
XX
PS Example 3; Page 36; 52pp; English.
XX
CC AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility
CC sequence (see AAR95443 and AAR95444) containing peptides. This sequence
CC corresponds to a region of dnaJ. These sequences are present on
CC arthritogenic proteins and are targeted in this invention as antibody
CC recognition sites. The anti-arthritogenic peptide antibodies that are
CC developed can then be administered to a patient who has RA or who is
CC predisposed to develop RA, to reduce the exposure to arthritogenic
CC peptides. The antibodies are produced and administered in milk. An
CC alternative treatment method comprises the administration of a non-
CC adsorbable antibiotic, together with a RA-beggn bacteria (selected from
CC the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the
CC patient who has RA (or a predisposition to it). Candidates for either of
CC these methods can be screened by detecting an in-vitro cellular immune
CC response to an arthritogenic peptide. The method of the invention allows
CC for the reduction of sensitisation to microbial arthritogenic peptides
CC (such as dnaJ). It also limits the exposure of the systemic immune system
CC of humans to RA arthritogenic peptides present in the gastrointestinal
CC tract
XX
SQ Sequence 15 AA;

Query Match 83.7%; Score 72; DB 2; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 KRAAYDQYGHAAFE 15
Db 2 ERAAYDQYGHAAFE 15

RESULT 12
AAM25796

ID AAW25796 standard; peptide; 15 AA.
XX AC AAW25796;
XX DT 06-APR-1998 (first entry)
XX DE Peptide dnaJpV which protects against arthritogenic peptides.
XX KW dnaJ protein; dnaJp1; adult rheumatoid arthritis; vaccine;
XX KW arthritogenic peptide; autoimmune disease; systemic immune system;
XX KW anti-dnaJp1 antibody; passive immunisation;
XX KW rheumatoid arthritis-susceptibility detection.
OS Synthetic.
OS Escherichia coli.
FH Key Location/Qualifiers
FT Misc-difference 1 /label= Q1D
FT /note= "wild type Gln substituted with Asp"
FT Misc-difference 2 /label= K2E
FT /note= "wild type Lys substituted with Glu"
XX WO9734002-A1.
XX 18-SEP-1997.
XX 20-FEB-1997; 97WO-US002957.
XX 15-MAR-1996; 96US-00618464.
XX (REGC) UNIV CALIFORNIA.
PI Carson DA, Albani S;
XX WPI; 1997-470882/43.
XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1
PT - also determining pre-disposition to rheumatoid arthritis by detecting
PT anti-arthritogenic peptide antibodies.
XX Disclosure; Page 5; 44pp; English.
XX Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
CC Escherichia coli. One peptide, dnaJp1 (AAW25795) was found to induce
CC relatively strong immune response in seropositive adult rheumatoid
CC arthritis patients. This peptide was used in a vaccine for protecting
CC against arthritogenic peptides. The vaccine contains a carrier, pure
CC dnaJp1 peptide or a recombinant gene expression vector encoding the
CC dnaJp1 peptide. The vaccines are used to prevent rheumatoid arthritis (or
CC other autoimmune diseases). Vaccines can target the arthritogenic
CC peptides before they are presented to the systemic immune system. Anti-
CC dnaJp1 antibodies can also be used for passive immunisation. Antibodies
CC can be used to detect rheumatoid arthritis-susceptibility sequences on
CC HLA or in populations of E. coli in the gastrointestinal tract
XX SQ Sequence 15 AA;
Query Match 83.7%; Score 72; DB 2; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
Db :|||||
2 ERAAYDQYGHAAFE 15
RESULT 13
AAE19458
ID AAE19458 standard; peptide; 15 AA.
XX AAE19458;

XX 31-MAY-2002 (first entry)
DT Heat shock protein (hsp) dnaJpV peptide.
DE
XX Human leukocyte antigen; HLA; DR-binding peptide; therapy;
KW stress protein; major histocompatibility complex; MHC; antiulcer;
KW type I diabetes; scleroderma; heat shock protein; hsp; vitiligo;
KW rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour;
KW ulcerative colitis; infectious disease; haemostatic; nephrotropic;
KW polymyositis; chronic active hepatitis; primary biliary cirrhosis;
KW pernicious anaemia; autoimmune thyroiditis; Sjogren's syndrome; cancer;
KW Grave's disease; autoimmune disease; multiple sclerosis; hepatotropic;
KW inflammatory bowel disease; Goodpasture's syndrome; neuroprotective;
KW antimicrobial; immunosuppressive; dermatological; antiinflammatory;
KW antiinfertility; idiopathic Addison's disease; cytostatic.
XX Unidentified.
OS
XX WO200212286-A2.
XX 14-FEB-2002.
XX 08-AUG-2001; 2001WO-US041656.
XX 09-AUG-2000; 2000US-0224104P.
XX 06-APR-2001; 2001US-00828574.
XX (UYCA-) UNIV CALIFORNIA SAN DIEGO.
XX Albani S, Prakken BJ;
XX WPI; 2002-227137/28.
XX Novel human leukocyte antigen pan DR-binding peptide, useful for treating
PT immune mediated diseases and conditions, has a fragment of stress protein
PT that binds to major histocompatibility complex class II molecules.
XX
PS Example 3; Page 46; 68pp; English.
XX The invention relates to human leukocyte antigen (HLA) pan DR-binding
CC peptide comprising a fragment of a stress protein that binds to one or
CC more major histocompatibility complex (MHC) class II molecules. The
CC invention also relates to heat shock protein (hsp) peptides. The peptides
CC of the invention and thr immunomodulating composition comprising these
CC peptides are useful for modulating, treating or preventing an immune-
CC mediated disease in a mammalian subject e.g. human, having or at risk of
CC having a disease including autoimmune disease, multiple sclerosis (MS),
CC rheumatoid arthritis, lupus erythematosus, myasthenia gravis, type I
CC diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma,
CC lymphoma, leukaemia, lung, liver, kidney, brain, bladder solid tumours,
CC retinoblastoma, sarcoma and connective tissue cancers) and infectious
CC diseases. The peptides of the invention are also useful for screening
CC peptides or analogues that modulate pathogenic immune response. These
CC peptides are useful for treating autoimmune diseases or disorders
CC including Sjogren's syndrome, polymyositis, chronic active hepatitis,
CC mixed connective tissue disease, vitiligo, idiopathic Addison's disease,
CC anaemia, autoimmune thyroiditis, idiopathic inflammatory bowel
CC gluten-sensitive enteropathy, Grave's disease, inflammatory bowel
CC disease, autoimmune neutropaenia, idiopathic thrombocytopenia purpura,
CC pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome,
CC bullous pemphigoid, discoid lupus and dense deposit disease. The present
CC sequence is hsp dnaJpV peptide used in the exemplification of the
CC invention
XX
SQ Sequence 15 AA;
Query Match 83.7%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 KRAAYDQYGHAAFE 15
:|||||

Db 2 ERAAYDQYGHAAFE 15

RESULT 14

ABR55133
ID ABR55133 standard; peptide; 15 AA.

XX

AC ABR55133;

XX

DT 03-JUL-2003 (first entry)

XX

DE E. coli dnaJpV antigen-specific epitope peptide.

XX

KW Antigen-specific epitope; immune response; T cell; cytokine;
KW antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;
KW cytotstatic; antithyroid; anti-asthmatic; immunosuppressive;
KW antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;
KW antiallergic; dermatological; antipsoriatic.

XX

OS Escherichia coli.

XX

PN WO2003026579-A2.

XX

PD 03-APR-2003.

XX

PF 25-SEP-2002; 2002WO-US030578.

XX

PR 25-SEP-2001; 2001US-0325499P.

XX

PR 11-DEC-2001; 2001US-0339284P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Albani S, Martins A;

XX

DR WPI; 2003-430097/40.

XX

PT Modulating an immune response in a subject having an immune-related
PT disorder, e.g. arthritis by administering an antigen-specific epitope and
PT a cytokine or an agent that effects cytokine activity or expression.

XX

PS Disclosure; Page 9; 41pp; English.

XX

CC The invention relates to a novel method for modulating an immune response
CC in a subject having an immune-related disorder. The method comprises: (a)
CC administering an antigen-specific epitope, where administration provides
CC epitope-specific T cell immune modulation; and (b) administering a
CC cytokine, an agent that effects cytokine activity or expression, or an
CC anticytokine therapy. The method of the invention has antiarthritic,
CC antidiabetic, neuroprotective, anti-inflammatory, cytotstatic,
CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-
CC ulcer, antianaemic, cardiant, respiratory general, antiallergic,
CC dermatological, and antipsoriatic activity. The method is useful for
CC modulating an immune response in a subject having an immune-related
CC disorder. The present sequence is used in the exemplification of the
CC invention

XX

SQ Sequence 15 AA;

Query Match 83.7%; Score 72; DB 6; Length 15;

Best Local Similarity 92.9%; Pred. No. 1.3e-05;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15

Db :|||||

2 ERAAYDQYGHAAFE 15

RESULT 15

AAR95445

ID AAR95445 standard; peptide; 14 AA.

XX

AC AAR95445;

XX

DT 01-JUL-1996 (first entry)

XX

DE RA susceptibility sequence peptide #1.

XX

KW Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody;
KW arthritogenic peptide; RA-begnnign bacteria; Escherichia; Lactococcus;
KW Klebsiella; Proteus; therapy.

XX

OS Escherichia coli.

XX

PH Key Location/Qualifiers

FT 1..5

FT /note= "rheumatoid arthritis susceptibility sequence"

XX

PN WO9531984-A1.

XX

PD 30-NOV-1995.

XX

PF 24-APR-1995; 95WO-US004896.

XX

PR 20-MAY-1994; 94US-00246988.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Carson DA, Salvatore A;

XX

DR WPI; 1996-020344/02.

XX

PT Treatment of rheumatoid arthritis - by limiting exposure of immune system
PT to arthritogenic peptide(s).

XX

PS Example 3; Page 36; 52pp; English.

XX

CC AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility
CC sequence (see AAR95443 and AAR95444) containing peptides. This sequence
CC corresponds to a region of dnaJ. These sequences are present on
CC arthritogenic proteins and are targeted in this invention as antibody
CC recognition sites. The anti-arthritogenic peptide antibodies that are
CC developed can then be administered to a patient who has RA or who is
CC predisposed to develop RA, to reduce the exposure to arthritogenic
CC peptides. The antibodies are produced and administered in milk. An
CC alternative treatment method comprises the administration of a non-
CC adsorbable antibiotic, together with a RA-begnnign bacteria (selected from
CC the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the
CC patient who has RA (or a predisposition to it). Candidates for either of
CC these methods can be screened by detecting an in-vitro cellular immune
CC response to an arthritogenic peptide. The method of the invention allows
CC for the reduction of sensitisation to microbial arthritogenic peptides
CC (such as dnaJ). It also limits the exposure of the systemic immune system
CC of humans to RA arthritogenic peptides present in the gastrointestinal
CC tract

XX

SQ Sequence 14 AA;

Query Match 75.0%; Score 64.5; DB 2; Length 14;

Best Local Similarity 93.3%; Pred. No. 0.00024;

Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QKRAAYDQYGHAAFE 15

Db :|||||

1 QKRAAYDQY-HAAFE 14

Search completed: March 7, 2005, 09:54:55

Job time : 160 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 09:58:03 ; Search time 130 Seconds
(without alignments) .
40.498 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 246509

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:**
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US10I_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	14	US-10-001-938-3
2	81	94.2	15	9	US-09-756-983-10
3	81	94.2	15	9	US-09-828-574-10
4	81	94.2	15	14	US-10-001-938-27
5	81	94.2	15	14	US-10-299-540-4
6	81	94.2	15	14	US-10-299-184-4
7	81	94.2	15	14	US-10-239-313A-444
8	81	94.2	16	14	US-10-239-313A-447
9	72	83.7	15	9	US-09-828-574-11
10	72	83.7	15	14	US-10-299-540-5
11	72	83.7	15	14	US-10-299-184-5
12	54	62.8	15	14	US-10-299-540-6
13	54	62.8	15	14	US-10-299-184-6

14	34	39.5	9	14	US-10-283-423-154	Sequence 154, App
15	34	39.5	9	14	US-10-283-423-155	Sequence 155, App
16	34	39.5	9	14	US-10-283-423-157	Sequence 157, App
17	34	39.5	9	14	US-10-283-423-158	Sequence 158, App
18	34	39.5	9	14	US-10-283-423-159	Sequence 159, App
19	34	39.5	9	14	US-10-213-821-154	Sequence 154, App
20	34	39.5	9	14	US-10-213-821-155	Sequence 155, App
21	34	39.5	9	14	US-10-213-821-157	Sequence 157, App
22	34	39.5	9	14	US-10-213-821-158	Sequence 158, App
23	34	39.5	9	14	US-10-213-821-159	Sequence 159, App
24	34	39.5	9	16	US-10-736-048-154	Sequence 154, App
25	34	39.5	9	16	US-10-736-048-155	Sequence 155, App
26	34	39.5	9	16	US-10-736-048-157	Sequence 157, App
27	34	39.5	9	16	US-10-736-048-158	Sequence 158, App
28	34	39.5	9	16	US-10-736-048-159	Sequence 159, App
29	34	39.5	14	14	US-10-161-959-6	Sequence 6, Appli
30	34	39.5	14	14	US-10-283-423-160	Sequence 160, App
31	34	39.5	14	14	US-10-213-821-160	Sequence 160, App
32	34	39.5	14	16	US-10-736-048-160	Sequence 160, App
33	34	39.5	14	17	US-10-845-407-6	Sequence 6, Appli
34	34	39.5	15	9	US-09-756-983-11	Sequence 11, Appl
35	34	39.5	15	14	US-10-161-959-5	Sequence 5, Appli
36	34	39.5	15	14	US-10-299-540-7	Sequence 7, Appli
37	34	39.5	15	14	US-10-299-540-8	Sequence 8, Appli
38	34	39.5	15	14	US-10-299-184-7	Sequence 7, Appli
39	34	39.5	15	14	US-10-299-184-8	Sequence 8, Appli
40	34	39.5	15	14	US-10-239-313A-443	Sequence 443, App
41	34	39.5	15	17	US-10-845-407-5	Sequence 5, Appli
42	32	37.2	13	15	US-10-089-887-58	Sequence 58, Appl
43	31	36.0	12	16	US-10-884-830-26	Sequence 26, Appl
44	31	36.0	12	16	US-10-884-830-285	Sequence 285, App
45	31	36.0	12	16	US-10-884-830-287	Sequence 287, App

ALIGNMENTS

RESULT 1

US-10-001-938-3
; Sequence 3, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3

Query Match 100.0%; Score 86; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFEQ 16
Db 1 QKRAAYDQYGHAAFEQ 16

RESULT 2
US-09-756-983-10

; Sequence 10, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJp1 heat shock protein
US-09-756-983-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3

US-09-828-574-10
; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKKEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaJp1 peptide
US-09-828-574-10

Query Match 94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 4

US-10-001-938-27
; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-27

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

US-10-299-540-4
; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTI
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-540-4

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
Db 1 QKRAAYDQYGHAAFE 15

RESULT 6

US-10-299-184-4
; Sequence 4, Application US/10299184

; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION
; TITLE OF INVENTION: AGAINST ARTHRITIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaJp1
US-10-299-184-4

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 7
US-10-239-313A-444
; Sequence 444, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-444

Query Match 94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 8
US-10-239-313A-447
; Sequence 447, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 447
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-447

Query Match 94.2%; Score 81; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
| | | | | | | | | | | | | | |
Db 1 QKRAAYDQYGHAAFE 15

RESULT 9
US-09-828-574-11
; Sequence 11, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKKE, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Irrelevant dnaJpV peptide
US-09-828-574-11

Query Match 83.7%; Score 72; DB 9; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
: | | | | | | | | | | | | | | |
Db 2 ERAAYDQYGHAAFE 15

RESULT 10
US-10-299-540-5
; Sequence 5, Application US/10299540

Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-540-5

Query Match 83.7%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 11
US-10-299-184-5
; Sequence 5, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant dnaJ peptide
US-10-299-184-5

Query Match 83.7%; Score 72; DB 14; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 12
US-10-299-540-6
; Sequence 6, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Bacterial dnaJp2 peptide
US-10-299-540-6

Query Match 62.8%; Score 54; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
:|||||
Db 6 QKRAAYDQYG 15

RESULT 13
US-10-299-184-6
; Sequence 6, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECTION IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-6
; CURRENT APPLICATION NUMBER: US/10/299,184
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 15

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OM protein - protein search, using sw model

Run on: March 7, 2005, 09:52:27 ; Search time 41 Seconds
(without alignments)
29.131 Million cell updates/sec

Title: US-10-001-938-3
Perfect score: 86
Sequence: 1 QKRAAYDQYGHAFFQ 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 171351

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	94.2	15	1	US-08-618-464-4
2	81	94.2	15	3	US-09-107-615-4
3	81	94.2	15	4	US-09-756-983-10
4	81	94.2	15	5	PCT-US95-04896-4
5	72	83.7	15	1	US-08-618-464-5
6	72	83.7	15	3	US-09-107-615-5
7	72	83.7	15	5	PCT-US95-04896-5
8	54	62.8	15	1	US-08-618-464-6
9	54	62.8	15	3	US-09-107-615-6
10	34	39.5	9	4	US-09-693-746-154
11	34	39.5	9	4	US-09-693-746-155
12	34	39.5	9	4	US-09-693-746-157
13	34	39.5	9	4	US-09-693-746-158
14	34	39.5	9	4	US-09-693-746-159
15	34	39.5	14	4	US-09-693-746-160
16	34	39.5	15	1	US-08-618-464-7
17	34	39.5	15	1	US-08-618-464-8
18	34	39.5	15	3	US-09-107-615-7
19	34	39.5	15	3	US-09-107-615-8
20	34	39.5	15	4	US-09-756-983-11
21	31	36.0	12	1	US-07-732-114A-5
22	31	36.0	12	1	US-08-170-114A-5
23	31	36.0	14	2	US-08-323-686-3
24	31	36.0	14	2	US-08-323-686-26
25	31	36.0	15	4	US-09-255-501-67
26	31	36.0	15	4	US-09-255-501-68
27	31	36.0	15	4	US-09-060-872A-67

28	31	36.0	15	4	US-09-060-872A-68	Sequence 68, Appl
29	31	36.0	15	4	US-09-500-135C-67	Sequence 67, Appl
30	31	36.0	15	4	US-09-500-135C-68	Sequence 68, Appl
31	30	34.9	9	4	US-09-721-870-180	Sequence 180, App
32	30	34.9	15	3	US-08-467-023-255	Sequence 255, App
33	28	32.6	11	3	US-08-467-580-14	Sequence 14, Appl
34	28	32.6	11	5	PCT-US95-08516-14	Sequence 14, Appl
35	28	32.6	15	2	US-08-521-871A-3	Sequence 3, Appl
36	27	31.4	12	1	US-07-732-114A-11	Sequence 11, Appl
37	27	31.4	12	1	US-08-170-114A-11	Sequence 11, Appl
38	27	31.4	13	1	US-08-487-568-45	Sequence 45, Appl
39	26	30.2	6	1	US-07-995-503A-12	Sequence 12, Appl
40	26	30.2	6	1	US-08-390-510-12	Sequence 12, Appl
41	26	30.2	6	1	US-08-390-790-12	Sequence 12, Appl
42	26	30.2	6	2	US-08-390-509-12	Sequence 12, Appl
43	26	30.2	6	3	US-09-149-860A-12	Sequence 12, Appl
44	26	30.2	12	1	US-07-995-503A-11	Sequence 11, Appl
45	26	30.2	12	1	US-08-390-510-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-08-618-464-4
; Sequence 4, Application US/08618464
; Patent No. 5773570

GENERAL INFORMATION:

APPLICANT: CARSON, DENNIS A.
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN IMMUNE PROTECTION AGAINST ARTHRITIS
TITLE OF INVENTION: INDUCING
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-08-618-464-4

Query Match

94.2%; Score 81; DB 1; Length 15;

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Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
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Db 1 QKRAAYDQYGHAAFE 15

RESULT 2
US-09-107-615-4
; Sequence 4, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-4

Query Match 94.2%; Score 81; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   |||||
Db 1 QKRAAYDQYGHAAFE 15

RESULT 3
US-09-756-983-10
; Sequence 10, Application US/09756983
; Patent No. 6787154
```

```
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10

Query Match 94.2%; Score 81; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFE 15
   |||||
Db 1 QKRAAYDQYGHAAFE 15

RESULT 4
PCT-US95-04896-4
; Sequence 4, Application PC/TUS9504896
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY
; APPLICANT: OF CALIFORNIA
; TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
; TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON
; STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04896
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: BERLINER, ROBERT
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-314
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-977-1001
; TELEFAX: 213-977-1003
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
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; CLONE: Immunogenic dnaJ Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
PCT-US95-04896-4

Query Match 94.2%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QKRAAYDQYGHAAFE 15
:|||||
Db 1 QKRAAYDQYGHAAFE 15

RESULT 5

US-08-618-464-5
; Sequence 5, Application US/08618464
; Patent No. 5773570

GENERAL INFORMATION:

APPLICANT: CARSON, DENNIS A.
APPLICANT: ALBANI, SALVATORE

TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN IMMUNE PROTECTION AGAINST ARTHRITIS

TITLE OF INVENTION: INDUCING

TITLE OF INVENTION: INVOLVED IN

TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CALIFORNIA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618,464

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/042001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: Immunogenic dnaJ Peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

US-08-618-464-5

Query Match

Best Local Similarity 83.7%; Score 72; DB 1; Length 15;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 6

US-09-107-615-5

; Sequence 5, Application US/09107615

; Patent No. 6153200

; GENERAL INFORMATION:

APPLICANT: CARSON, DENNIS A.

APPLICANT: ALBANI, SALVATORE

TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN

TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST

TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN

TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CALIFORNIA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,615

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/618,464

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: HOWELLS, STACY L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07340/042001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: Immunogenic dnaJ Peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

US-09-107-615-5

Query Match

Best Local Similarity 83.7%; Score 72; DB 3; Length 15;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 7

PCT-US95-04896-5

; Sequence 5, Application PC/TUS9504896

; GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY

APPLICANT: OF CALIFORNIA

TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT

TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBBINS, BERLINER & CARSON

STREET: 201 N. FIGUEROA STREET, 5TH FLOOR

;; CITY: LOS ANGELES
;; STATE: CALIFORNIA
;; COUNTRY: US
;; ZIP: 90012
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04896
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BERLINER, ROBERT
;; REGISTRATION NUMBER: 20,121
;; REFERENCE/DOCKET NUMBER: 5555-314
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 213-977-1001
;; TELEFAX: 213-977-1003
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: Immunogenic dnaJ Peptide
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..15
;; PCT-US95-04896-5

Query Match 83.7%; Score 72; DB 5; Length 15;
Best Local Similarity 92.9%; Pred. No. 3.1e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 KRAAYDQYGHAAFE 15
:|||||
Db 2 ERAAYDQYGHAAFE 15

RESULT 8
US-08-618-464-6
; Sequence 6, Application US/08618464
; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS
; TITLE OF INVENTION: INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.

;; REGISTRATION NUMBER: 34,842
;; REFERENCE/DOCKET NUMBER: 07340/042001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619/678-5070
;; TELEFAX: 619/678-5099
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; IMMEDIATE SOURCE:
;; CLONE: dnaJp2
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1..15
;; US-08-618-464-6

Query Match 62.8%; Score 54; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
|||||
Db 6 QKRAAYDQYG 15

RESULT 9
US-09-107-615-6
; Sequence 6, Application US/09107615
; Patent No. 6153200
; GENERAL INFORMATION:
; APPLICANT: CARSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
; TITLE OF INVENTION: INDUCING IMMUNE PROTECTION AGAINST
; TITLE OF INVENTION: ARTHRITIC PEPTIDES INVOLVED IN
; TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,615
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,464
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWELLS, STACY L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07340/042001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; IMMEDIATE SOURCE:
; CLONE: dnaJp2
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-6
Query Match 62.8%; Score 54; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYG 10
Db 6 QKRAAYDQYG 15

RESULT 10
US-09-693-746-154
; Sequence 154, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-154
Query Match 39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 1 FDDYGHLERF 9

RESULT 11
US-09-693-746-155
; Sequence 155, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
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; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-155
Query Match 39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 1 FDDYGHLERF 9

RESULT 12
US-09-693-746-157
; Sequence 157, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-157
Query Match 39.5%; Score 34; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
Db 1 FDDYGHLERF 9

RESULT 13
US-09-693-746-158
; Sequence 158, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-158
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Query Match
Best Local Similarity 39.5%; Score 34; DB 4; Length 9;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:| ||| |
Db 1 FDDYGHMRF 9

RESULT 14
US-09-693-746-159
; Sequence 159, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-159

Query Match
Best Local Similarity 39.5%; Score 34; DB 4; Length 9;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:| ||| |
Db 1 FDDYGHMRF 9

RESULT 15
US-09-693-746-160
; Sequence 160, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method
; FILE REFERENCE: 6297.lcp
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-160

Query Match
Best Local Similarity 39.5%; Score 34; DB 4; Length 14;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:| ||| |
Db 1 FDDYGHMRF 9

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAF 14
:| ||| |
Db 6 FDDYGHMRF 14

Search completed: March 7, 2005, 10:07:26
Job time : 41 secs